GGTGCGCAAA GGTTACCTTA GAGTGGTTGG AAATCACTCT GTAAGTGTAA AGGCATAAGG   2760

TAGCTTAACT GTAAGACTGA CAAGTCGAAC AGATACGAAA GTAGGTCTTA GTGATCTGGC   2820

GGTGGCAAGT GGAAGCGCCG TCACTTAACG AATAAAAGGT ACTCCGGGGA TAACAGGCTT   2880

ATCCTTCCCA AGAGTTCACA TCGACGGAAG GGTTTGGCAC CTCGATGTCG GCTCATCGCA   2940

TCCTAGGGCT GGAGCAGGTC CTAAGGGTAT GGCTGTTCGC CATTTAAAGC GGTACGCGAG   3000

CTGGGTTCAG AACGTCGTGA GACAGTTTGG TCCCTATCTG CCACAAGCGT TGGATATTTG   3060

AGAGGAGCTA TCTTTAGTAC GAGAGGACCG AGATGGACGA ACCTCTAGTG TrCCAGTTAT   3120

CCTGCCAAGG GTAAGTGCTG GGTAGCTACG TTCGGAAAGG ATAACCGCTG AAAGCATCTA   3180

AGTGGGAAGC CTTCCTCAAG ATGAGATATC CTTTAAGGGT CCTGGAAGAA TACCAGGTTG   3240

ATAGGTTAGA AGTGTAAGTA TAGCAATATA TTAAGCTGAC TAATACTAAT TACCCGTATC   3300

TTTGGCCATA TTTTTGTCTT CCTTGTAAAA ACCCTGGTGG TTAAAGAAAA GAGGAAACAC   3360

CTGTTATCAT TCCGAACACA GAAGTTAAGC TCTTATTC   3398

(2) INFORMATION FOR SEQ ID NO: 36:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 3203 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GAGAAACCAA GAATTAAATG TAAAAATAAA GATCGTTTCA TAAAGATTGA AAAAGAAAAT   60

GACAAAACAA TGTATCATAC AAAAATAATG ATGGATATTT ATAAATTAGG AATTGACAAT   120

AAAAGAAATG AATGTCGTAT ATCATTAAGA ACACTATTTA ATCAAATGAA AGTAGAAGAA   180

GTTCGTTTAT ATTCTATAAA AGAAGGGGAC AAATTTTTAG GTATTTACTA TGGATATAGA   240

AAACCTATAA AAAACATTTT CGTAAAATAT GAAATAAACG GAACCATAAA GTCATATGGA   300

TTATCAAAAG CACATTACAT AGAATTTAGA TTTAAAAAAG GAAGCGTTTT TTGTTACTTT   360

AAAGGATTAT TTCGCTTATT AAAAAAAGAA AAAGAAATA CACCATATAA TATGGCTTGT   420

ATTGATATGT TTACAAAACT AGAGAAACAC GTATATGAAT TTTACGGTAA AAAATATCCA   480

GAAAAAGGAA TAATTATAAG ATGGATAGAA AAAAATCAAA AATAATAACA ATTGCAAGCC   540

TTAAAGGGGG CGTTGGTAAA AGCACAACTT CAATAATACT TGCAAATCTA TTATCGAAAA   600

AGCATAAAGT ACTTTTGATC GATACAGATG ATCAAGCTGC TACTACAAGC TATTATTATA   660

1001

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ATGAATTAGA AACAAAAAAT TTCGATATAT CTAAAATGAA CATAGGAAAT GTTATAAAAG     720

ACGGTACAGA TATTAATAAA AGCATTATTA ATGTTGAAAA TAACATAGCT TTGATACCCA     780

GTTATATAAC AGTCGATGAA TTAAATGGAG AGTATTATTA TGATAACCGG CATCTTCCAA     840

TTGAATTTTC ATTAAAGACG AAATTAAATT CCATAGCAGA CAACTATGAT TATATTATAA     900

TTGATACTAA TCCCAAAAGG AATTTCACAT TAAAGCTTTC CCTAATTAGC AGTAATTATG     960

TAATATCTCC AATGACGGCA GAAAAATGGG CAGTTGAAGG ATTTGAAACA TTAAGAAGGT    1020

ATATAAAGA AGTTGCTGGA ATACCAATAT TTATTGTTAT TACAAGGTTT AAAAAAAATG     1080

TTACCCACAA GCAATTAATG GAAATAGTAA GCATGAAAAA CGGGTTTTTG GGATACATAA    1140

GCGAAAGAGA AGATTTAAAT AAAAGAATAG GGTGTAATGA AAAATTTGAT TTTTCAAAAG    1200

ATTACATTAT TGAATATAAA AAAATATTGG ATGTTTTTTT GGGAAAATTG TAAGAATTGA    1260

CAAACTTAAT AAGTCCGGCA TGCCGGACTT ATTGGAAATA AGGGCAAAAA TATGAATAAA    1320

AAAAACATTA ATTTAAAAAT TAATAAAAGA ATTTCAGAAA ATAATTTAAA TTATATTCTT    1380

GATCAAAGCA ATGAGAATCA AAGAAAGAA GAATTTGAGC GATTAATTAC ACAATTAAAA     1440

AATAATATTA AATCAGAAAT ATACAATATT ATTGATACCA TGAAGATCCT TAAGAAAATA    1500

AATGACAAGA GGCTCTATTT AGAAGGAGGA TATAAATCTT TTAAAGATTT TTTATCAGAT    1560

TTTAAATTAG CAAAGACACA GTCTTATGAA TATATAAAAT TAGCCGCTGC AATTGAGGCG    1620

GGAATATTAG AAAGAAAATT TTATTACCAA TAATGGAATA AGGGCCTCTA TAAGATATAT    1680

TAAAAATCAA GCAAATGGTA CAATAAAAAA ATCAAAACAA AATCCAATAA AACCATTAAG    1740

ATTTCAACTC AAGAACCAGG AAAGTTATGA CTTTTATAAA AGCAATTCTA GGTTTGTAAG    1800

TTTTATGATG GATGAGATTT TTAAAAATCA AAAAGATTTT CTTAATAAAC TTTTAAAAAG    1860

ATATAAGGAA TCAAAGGGAC AATAAGAAAA TTTTATAAGC AATTTAATCT TTAATATTAT    1920

TGAAATATAA AATATAAAGT TAGAAATTGT AAATAATTGA TTTAACAAAT AAGGAAATAT    1980

ATACAAAAAA GCAACTGAAA ATTTAAAAGA TCATTTGCTA AGCAGAGGAA TTTTATTTGG    2040

TTAAAGTATT TGAAAAAAAA TTAAATATTA TCAAAGAAAA AGGTAAATTG ATCTCAATTG    2100

ACAATAAATT GTCAGTAATA AGCAACGAAG AATGTTTTTA ATTTTGATTA TAATAAATTT    2160

TGCAAAGAAG CACGCTTAAT AAGCACGGTG TAATAAGTTG GGCAATATCT TGATTAGCAA    2220

CAATGTGTTT TGATAATCAA TGGTAAGACG AACACTTAAA AATATTTTAG AAGGAACAGG    2280

GCATTTAAAG TAAATTTATA TATATTTAAG AGTAAGGATT TGAATAATTT ATGATTTAGA    2340

GCTGTAGAAT TTATTAAAAT ACAAGAGCAA CTATTAAAAA AATGGGCAAA TTAGAAACTT    2400

TAGCAGGGGT AGTGATTTAT AAGGACGGGG TGTTAATGAC GATATTATAT AGGCTCAAGG    2460
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GCCAGCAAGG ACTACTATTG ATTATATAAA CACTGTTGTT TAAGATTTTA AAAAAAAGAG   2520

GCTATTTTAA AATAACAAAT ATTTTATAGA ATTTATATTC AAGCATAAAT TTAGGAATTA   2580

AAATCAATGA GTTTACTATG AATCTTGAAT TTGTTTTGTT AAATTCAAAA CCACCACACC   2640

CCTATTTTTT AGCTATCTAA TTAAGGGATC CATATGTGTC CCCTTTATTT TTAAATAAAA   2700

GATATATATT TAAAGACAGT TAGGCCTCTT TTAGGCATAT TTTTGTTTAA TAAAAAATAT   2760

TAAATTAGGG TTTATAATTT TTATAGATGA AAATAAAATA GAAGAATCTA ATTTAACTAA   2820

ACAATTTTTG TTTAGTTAAA ATGATATAGG GCTTTGCAAA GTAGATATAA TTAAAGAAAA   2880

TCTAAAATCG CTAAATAAAA CTATTTAAAC TAAGCCCCAT AATGAAAAAG TTTTAGTAAA   2940

AATATTAAAG AATATTTTTA CTAAAATAAA AATTAAACCA GCATTAATAA TACTTACATT   3000

AGATGATTAG CTACTTTTTT TAATTAATAA ATTTTGCATT TAAAGTTCTA TTCCACTTAT   3060

AAATATTGAC TATATCAATA ATTTTTCAAG CATTGGTACA TTTTATATTC TAAATATTTC   3120

GTTTTGTCGC TAATTTGTTG ACATAGGAAT TATAAAAAGG CCATCATCTT TTAAATTAAA   3180

  3203

AAGTAAAATA ATACTAATAA ATA

(2) INFORMATION FOR SEQ ID NO: 37:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3189 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TTGCTAAAAA TATATTTTTT TATATCTtGG CTCTACTACA ACTCCTTTAT TTTTAGAGTA   60

ATAAATAAAT CTGCTGCCAA ATAACCTATA AGATATTTTT TAAACATAAC TTGGATCGAT   120

ATTTATAGAT TTAAAAATTT TTAAATCTAT AATAACTTCC AAAATACAGA ATCTTCACCT   180

AGATTATAAT TGTTTATAGC ATATTCTTCT TTTGAATATG TAAATTCTTA AGCTTATTTA   240

AAAGCTTTTT TCTTGTATAG TCAATTAGCT ATTTTAGCTT TTCTGGTTTG AACGCCAATA   300

CTAAAATTAT TGAAAATATC TTTTAAAGAA ATCCCATTGT CATAAATATC TTTATTTGAA   360

AAATCTTTTT AGTAAAAAAA TAATGGGGAT ATTTGTATTC AAGTTTTTCA AAATTAATAG   420

TAAAGATATT GTTTTTTCCT AAAAACCCAT ATTTTTTTTC TCTTTTGCCT TTAATACTTT   480

TGTAAAATAC TTTAATCAGC TTACTTTTTT TAGTCCATCT TATATTTAGT AAAAAATAGCA   540

ATAGTAACTC CGGTTTGGAT ACAAAATACA TTCTCACCTA TACTGCCATC ATCAGTTTTT   600

TTCTTTCTTG AACTATCGTG TAAATTTAAT ATATAAATTT CATCAAATGT TTTTAAGAGG   660

TAATCTCATA CCTCTGAATG CCACCTTGTC AAGGTATCCA TTTGTTTGTT ATGATACCTA   720

GCAATCCTtC GTTAGAACTT TTAATTCTAT GTTCTGCAAA TCTAATAAAC TTAGTGCGGT   780

CATCATTAAG TGGCCTTAAA TTTTTTTCAT TTATAAACTT ATTTTCTATT TTTTTATAAT   840

CATTAACTAA ATTTAATATA TATTCATTAT TATTTTTTGA ATCTGAATTA TAAGGAGGAT   900

TTCCCAGTAT GACAAGTATT TGCTTTTCTT TAGCTTTATT TGTAAGTTTA TTTTCTTCTC   960

CAATTGCAGG GAAAATACCT TAAAAGATTT TTGATCTGAA GGGTCTGCTT TATCAATAAA   1020

ATTAGTCAAA AATATTTATA ACTTTATGTT TTCATTATTT AAGCTGTCGC TACAAATTTT   1080

TCTTTCAAAT ATTGACTTGG CTTTAAATGA TCAACTACAT AAGGAACCAT TAAACATTCA   1140

AAACCATAGA CATTTTTAAG TATGTGAAAA TTAATGTAAT CTTCTTGTTT TTCAGAGTCT   1200

ATTGGAATTT CGTTTAATAT AATTTTAATT ACTTCAGGTA AAAATGTGCC AATACTTATT   1260

ACAAAATCAA ACACTGCAAC TTTATCCCTA TTTTTAAAGC CATAATTTAA TTTAATTTTT   1320

TTAAGTGCCT TATGTAAACT GTTAACAATA AAACTTACAC CCGAATAGGA AGTGTACTAC   1380

ACTCCTTTGG CCTTTCTTAA TTTAACATCG TACTTAGCTA GAAAATCCTC ATAAAAATAA   1440

AGATAGGGGA TCTTTTGAGC TTGTTTTGGC TCTTGTAAAA GAAAATTCTT TAAAAAATAA   1500

GCTCTGTATC AATTTATTTA TTACATTAAT AATTTCTTCT AAAATCTATC TTGGACTATT   1560

ATATTCATTA TTTGTATCAA TATCACTAAT TAATTTTAAT ATATCTCTTA TAAGCGAAAA   1620

GTTAGAAAGT ATAAACTTTT TAATATTATA AAAAGCTATT TTTCATTAAA TTTAAGCAAA   1680

GACATAATTA CCTTATCTTA AACTTTTAGA TAATTATAAT TGATTTTTAA GGAAATCAAA   1740

ATGATGCCCC AAAAGCTTTT AATAATAAAA AATTGTTATT CTTGCCAAAA GCTACTTAAG   1800

AAAAATAGTA AAATTTGTTG TGTTGTTTAT AGAACTAGAA ATAAATACCC CAAAACCCTT   1860

ATAACGAGCT AATAATTGTT TTTATTGGGA GGTTATTTAG GGATTGTAAA TTTTTATATA   1920

CAAAGCCTAA AACAAATTTT ACATTTTTAT ACTCATATCC TTTTCTATTT CTTGCTTGCT   1980

GTTTCTTTAT AATAACGAGT TTTTAATCAA TTAAATAAA ATTTTTCTTT CTAACATCTT   2040

TCTTTCTTCT TTCAAACCAT CTTCmAGACA CTTTAATTTA TCTTTATAAC TCTTCtTTAT   2100

CTTTTGGTTA TTCtTCtTTT TTAAATTTcT CTTACTTTTT GTATTcTTTT TCAATCTTTT   2160

CTAATTCTTG TATtCCTTTT TTATTAACTT CTAATCTTAG ATTTTCAACA ATATTTTAAG   2220

CTACCAGATT TTTAGATTTC TCTTGTATCT CTGCTTGGCA TCTTAAATTA ATTTCTCTTT   2280

TATCTCTTCT TTTGTATCTA TAAAATCTAA AAATTCTTTA GCTTGTTTTT TTAAATCTTA   2340

TTCTAAATTT TGTATATCTA CAACTTATAT AATGTTTATA AGAACTTATT AATATAAAAA   2400

TAGCAGACAT AGTAAACTTT TCCTCATAAT TATCCCACCA AGCTTTAGGA ATATATTAAA   2460

TACCTATATT TACATATATA AAGCTTAAAA GCAATTTAAT TACATTGCAC ACTATAAAGC   2520

AAAAAAATAA AGCCCAAAAA AACTACTCCC CCCAGAGCAC AAATTCCAAA ATCACCAAAG   2580

CAGATCACAA TAAAGACAAT TAAATGCAAA CAATAAAAAT ACAAGATATT CCAACTTTAT   2640

TTAATAAAGT TGGAATAATT TTTTGCAACA TAAATTTTGA AAGCATTATC AAAATAAACA   2700

TTTATTAATA AAATTGTAAA AAAGAAAAAC CGATATTAAA TACAAAGCTC AAATATCTAT   2760

AAGTTAATTT AGTTTTACAA CAACTAGCAA TAAAACTACA TTAATAAAAT TAATAGATAC   2820

ATTAAATTTC AAATCTTCAT TACAGACACT ATAAAACAAA ATTTTGTATT TTACTTTTTC   2880

TTATTATTAT ATTAGTTACA ATATCAAGCA AAACATCTTT TCTATTCTAA AAAGCTCCTT   2940

AAAAATATAA TTTACTATTA TTATCTCTTT TTTACAAACT CACATAATTC TTTATCTCTC   3000

ATGAAAATTC TAATAGAAAT ATTCTTATTA TTTAATTTAC TTATATGATT ATTAAAATTT   3060

AATGATTTTT TTTCTAAACA TGTGTTTTTT TATATTTTTA AATCCTAATT CCTTAATCTT   3120

ATCAATAGAT AAAACTATCC TCCAAAACTT TTGACTAAAG TTTTAAATAA AAATAAGTTT   3180

                                                                     3189

GCnTTTAGC

(2) INFORMATION FOR SEQ ID NO: 38:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 3130 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTGTAAAAAG TTTTGTTTGA TATAAGTTCA CTTGTGCCCT TTACTATTTT TGTAGTTGCT   60

TTTACTTTCA GCTTCATTAG CAGTTGCAAG TTTTTTCATA CATTCATAGT AAAGCTCCAT   120

TTCTCTTATT GAACACTCCT TTATATATTC ATCAAGCTCG CTTTTTAAAG AATTAATTTC   180

TCCATTAACA ACTTGCTTAT TTTTTTTACT ACTTGCTTTA TTTAAAGCGT CAATTTCAGC   240

TCTTAAATTT TCTATTTTAG TATGCATACT AAAAAGCTCA ACACTAGAAT ATTGCTTAAA   300

TGCATTTATA AATCCTAATT CTAAATTAGC CCGCTCTAAA TCCAATTCGC TTCTAACTTT   360

CCTAGCGTTA ACTTCTGATT TAAAAGTTTG CGACAAAAGG TGTTCAAAAG TGTCTTCACT   420

AATTGATAAT CTAGAGTCAT CGCTAACAGA ATTTTCCCCA CTTTCCCATT TTTTCCTCAT   480

CCTCCACACA TTTACCCTAG AAACCCCCAA TTTATCCGCT ATTTCCCTAT CATCTAACAA   540

1005

TCCTTCTCTA AAATATGCAA CATAATCATC AAAAGACCTT TTAACTTTTT TCAAAAAATC   600

CTCTAAAATA ACAAAATTAA CAAATTGTTG CTCTAAATAG TAAAGCAATT TATCAATTGT   660

TAACATTAAC TATTGTCTTG TTGATATCTA TTGACCACAG ATCTATCTTT ACAATTCTTA   720

TTAAACATGA ACCAGTATCA TTATTGTCGC CATTAAGAAG ACCCCTCATA AATTCGTTAG   780

CATTTAAAGA AAATAAAGCA AATATAAAAT AATATAAATT CTTTTTATTT ATCATGATTC   840

TCCAATATTA ATAAAATAAC AAGACTAGTA GCTAATCTTG TTATTCATAA TTTATGCTTA   900

TAAAAACCAT TTATTTTATT TCGAAATCTT TTTTAGCTTT TCTTAATAAA TATCTTATAA   960

GATTCTTTTT TCAAATTAAA ATCTAATCTT TGGGCAAATC AGCCAAAATT TGTTTTAAAA   1020

TTTGTTTAAC TGTATTTGCT TTATCTTCAG AATAATCTTT TTTAAAATTA TTTCTGGCGT   1080

TATCTCCATA TTTCTCAGCA TAATCAATTT TATCCGAATT TAATTGTATC AAATAATTAA   1140

AAATCGAATC TGGATAACTC CCTATAAGTC TAATCATATC CTCAGACAGG AAAATACTAT   1200

CAGTACTTAT CTTAATTTTT ATAAGATATT CAATAGCCTC AAGAGCGTCC AAAAAAACAC   1260

TTTTTTCTTT AATTCCAATT TTTCTTAAAT CTCCTCTAAT TCTAGGAGCA TCGGAAAAAA   1320

CATGACTTTT TTCATACTCA TTTTTAAAAT CATAATTATC TAGTCTTTTA TTTATTAGGT   1380

TAAAATCTTC TTTAGAAAAA GCTCTTTTAG TTTCTGTATA ATTTTCTTCT ATATTTGCAC   1440

TTAAACTTAC TACAAATAAA AACAAAAATA TTAACAGACT AATTTTTTTC ATATCCCCTC   1500

CTAGCTTTAT TGCCTAAATT TCAGCAATGT AAATGCTAAT AAACAATAAG ACTGATTGTT   1560

AGTCTTGTTG TTTATAATTT TTACTATCAA AACCCATTTT TTATTATTTT TTATCTTCTA   1620

TATTTTGAGG CTCTGCTAGC TTTTCAAGTT CTTCCTCAAT ATTTTTAAGA GCATCATCTA   1680

TAACCTTTTT TACAAAATCA TTAGTATTAG TACCATCATT AACAGAATAA CTTCCATTTA   1740

CACCCAATTC TTTAGCATAC TTTAAAGCTT TTTGTCCAAT ATTTCCTTGT TTTTTAACTT   1800

TCTCAGTACT TTCTCCAGTT GCAGATTCAA CTTGTTCTTT AAATTCTTGA AATTTCTTTC   1860

TAGCCTCTTC TAATTCTTTT TTTCTTTTAT CTATTTTATC CTTTAATTCT TGAATTTCTT   1920

TTTCTTTCTC TTCTTTTCCT TCTTGTTGAC CACCATCTTT TGCTTGCACC GCTTTTAATA   1980

CGGGTGTGTT ATCGTGGGAA CTTGCCGGCA ATACTGGTGG TGGATTAAAC AGACTGTTAT   2040

TAGGATCGTC ACCTTGCATT AACTCTTTAT CTAAAAATCC TTCAACTTTT TCTTTTACAT   2100

TTTGTTTTAA ATCTTCACTA CTCGCATCAA TCTTGCAAGA AATTATCAAA ACAAAAACTG   2160

CACAAATAAT TAAATTTTTC ATTTTCTTAT TCATAAGTTA CTCCATAAAG TACTAATATT   2220

ACCACAACAC CAAATAATTG CAATATTTCA AAGATTTAAA TATATAATTT TGTTACATTC   2280

AGCTGTTACA TTTTAACAAA ACACAAATGT AATTTTAACC AACTCGCCAA AATCTCTCCA   2340

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TTGCAAATGC TCTACTCATT ACAAAGATT ATAAAATACA TACAAATTAA ATTTTCAAGT    2400

CTTTGCTATA TATTACACAA AGTATACTAT CTTTCTTGTG TACCACCCTC AAAAATCACT    2460

ACTTCTGTTT ATTACACCCA CTCTACAGCC CAGATTTTGC ATGCAATGAG AACACTCCAA    2520

ATTTGACTAA AATTTTTCGT TTTTAGTAAA ATATAATTTA CATTTTTTAT CTATTTTTAT    2580

TACTTTTACT TAATTTAAAA GTAACAACTT CAAGGAGAGG ATTTTATGGA CAATAATAAT    2640

TCTTTTAATT TAAATAATTT CAATATGGAT TTTACGCTCA AACTATTTCA AGAATACCAA    2700

AAACTAATAA ATGAAAACAA AATTCTTAAA AATTCACTAA AAAATTCATC TAAAAGTAAA    2760

AAAGAAAATT CAAAACCAAC TCCTAAGTTT TATTTAACCC CTAAAAGTAT TAAATTAATT    2820

CTAAAATGTG CCAAAACCTT AAAACAAATT GACCCAATTT CTGGTTGGTT TGTGCATCTA    2880

CTCTTAATAA GTGGATGTAG AGGCACTGAA ATGCAAAAAG TAAAAATGCA AGATATTTCA    2940

ACTTTTTTAA GCAAAACCGG AAAAACTTTA TATACTATTA AAGTAAATGT GGCAAAAAAA    3000

AGAAATACCT CTTGTATTAG AGAAATTGTC ATCAACTCAG AAGAGTTCGA GGCTATCCAA    3060

ACAGCACATA AAAATCATTT CCAAGAAAAA ACTCTTGACT CAAGGCGTAC TTATCTTTTC    3120

CAAAAGAGCA                                                          3130
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(2) INFORMATION FOR SEQ ID NO: 39:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 3029 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

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AGTTTTCCCA TTTCGCTCCG TAACTTGTGA TTACACTATC ATTTGmGwcy CCTGATATkT    60

cTGTGGAkaT TATTGTTgAA GmTTTTCCtC TTTTcCTCCT TATTTTGTAa TAAaTAtTAT    120

ATgCAAAAAC TATTTTTGCC AACTTTTTTA CAAAAAATTT TACAAAAAAT TAGTTGGGCT    180

TATTTAAATT CTCTTGTTAA AGAACTTAGC TAAACCCAAC TTAATTGGAT TTTTTTGATA    240

GCAATATATT TTTTTAGTTA TACATATACA TATGTATAAC TAAAACTATT TTTGTCAGGC    300

TTTTTACAGA AATTATTATA ATAAATAAAA GCTTTATTAA ATTCTCATGT TAAAGAGCTT    360

AATAAAGCCG CGGGCTTAGC TTAATTTATT TTAGATAAAC TCACTAAACA ATTAAATTCA    420

GTTCAATTTA GAATTAAAAT TATTTTGTAT TTATTAAAAT AAAAGAACCT ATTTAAATTA    480

TCTTGTTAAA AAATTCAAAT AAGTTCTACT TTAGAGCTAT ATACTAACTT ATTACTTTAT    540
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1007

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AAAATTTTAA TCATTTTCAA TTGAAAAAAC ACTTATTAAA TATAGAATAG ATAATTGGGG      600

CAAACGTTAT TCCCATTATT AGAATTACTT GTATTGTTCT ATTGCTTGCA TTAAGTTCAT      660

TTTTTTAAAT ATCTATTTTA TTGTCTAGAC TAGATATATC TTTTTGCAAA GTTTTTTCTA      720

CACTATCTAT TTTAGTATTT ACACTATCTA TATCTTTTTG AAAATTCTTT TCTACATTAA      780

TTATTTGTTG TTCTAAAGAA TTCATTTTCT CCTTTAAAAC TTCAAAGTTG TAATTGTCGT      840

TCTGAAGTAA AACAAAATCT ATTGCCTCTT CACTAAACCC CTTATTTAAA AATTCTAACC      900

TTATATTTTC TATTTTAAGA GCATTGTAGG CTAAATTACT CATAAATCC CCTTTATTAT       960

CCTTTTAATT CTTTATATTT TTTTAAAAGT TTATTAATCA AATCTTTTTG ATTTTCAAAA     1020

ATCTCGTCCA TCATAAAACT AGTAAATTTG GCATTTTTT TATAAAAATT ATAACTTTCC      1080

TGTTTTTTAA GTTGAAATCT TAGGGGTTTT ATTGGATTTT GCTTTGACTT ATCCTCTTTA    1140

ATTTCTACGT TTAATATATT TCTATATACA CCCTTTAAGC CTTTTTCTTT AATATCATTT     1200

ATTGATATGC TCCCCTCTAA TACTTTTCTA TAAATTTTAA GGTATAAAAA AGCCTGACTT     1260

CTAGATATTA TAAATTCTGA CAAAAAGTCT TCAAATTTTT TATAACCATC AATCAAATAA     1320

AGTTTTTTTT CTCTTATTTT ATATAGGATT TTCATTGTTT TAATTTTATT CTCAACATCA     1380

TCAACAGTAA TTCTACGAAG TTGATCCTTA TAGCTTTTAT ATTCAAGTTC CTCATTTTCA     1440

AATTCTTGAA CATCCTCAAT TCTATTATTT AATAATATTT TTTTTACTTT TAACTTTGAC     1500

ACTTAATCCT CCTAAGTTTC TGATTTATTT TTAAAGTCT TCCGGAAGAC TTTTAAAACA      1560

TATTGTTTAA TATTTTTTTT ATTTCTTGAT AATAAATTTC TTTATTATTA GGCTCTTTCA     1620

ATTCATTTAT AAAAACCTTA ATTGAATTAT AAAAATGAAC TCTTCCTTTA ATAAGATCTT     1680

TGTATTCTGA CTGCAAAATA CTTTCAATAT CTTTATACGT ATTTCTATTT TTTATAAATT     1740

GATTTCTAT TATTAACACA TCAATATTTT TCTTTCTTAT TATTTCAACT TCCTTTATTT      1800

CATTCATTAA TATTGGCAAA GACTCTACAG ACCACCTTTC TGCTTGAATA GGTATTATAA     1860

CTTTATGTGT AATGTTTAAC GCATTAAACA ATAAGAACT TAAACTAGGG GGAGTATCAA      1920

TTACTACATA ATCAAAATTA TAATAATGTA AATTTTTATC AAATATATGT TCTAACATAA     1980

GCTCTTTATA AGGAATATCT CCTTTTTCAA ATTTACATAA AATTGGATGG GCCGGAATAA     2040

TATACATATT ATTATTTATT GAATTTATAT ATTCATTAAA AGCAATGTTT TGATCTCTTT     2100

TTAAAGATA ATAAACATTA TTCAATTCAA TATTTCTGAT ATATTGTAAA AAATAACTGG      2160

TTAAACTATT TTGAGGATCT AAATCTACAA TCAACACTTT ATTGTTCATT TCGCTTAAAA     2220

TATATGAAAA TATAATTGAC AACATGCTTT TGCCAACACC GCCCTTAATT GACGCTATTG     2280

TTATTATTTT AGGTTTTTTA TTATCCATTT TATTAACGGT CCTTGTTCTG GGTATTTTTT     2340
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CCCATAAAAT TTATATACTT GTTGTTCTAA ATCTGTAAAC ATACTAAATA AAACTTTGTT   2400

GTAATGATTA TTTGTTCTTT TTTTATCTAA TAATCGATAT AATCCCTTGA AATAGCAAAA   2460

TACACTTCCG GCTTTAAATC TAAATTCCAT ATAATATGCC CTTGCTAATG CATATGCTTT   2520

TCTAGTTCCr TTTATTTkAT ACTTTATTAA wGGyTTTTTn ATTGGTTTTC TrTAGCCATA   2580

AAAAATACCA ATAAACTTAT CTCCTTCTTT AATTGGGTAy AArTGAGTTT CTTCAACAAT   2640

yCTTTCCCCA TTAAATAGGG CCCTTAATGA TAGTCTAAAT TCATGTTTTT TTTCATATAC   2700

TCCAAATTTG TAAATGTCCA TCATTATTTT TGTATGGTAC ATTGCTTTAC CATTTTCTTT   2760

TTCAATTAAA ATAAAGCGTT CTTTATTTTG ACATTCAACT TTACATTTGC CCTTTTTTAT   2820

AGTTTCAATA GGCTCCATTG CACTTTCCAT ATTTAAATCC TCATATAGCC TTTATGTTAA   2880

ATTCTTCTGT GGTTAAAGAA TTTTTTTGTT TTCTTATTAT TTCCAATAAT TCAAGATAAT   2940

ATGTACCAAA TACTTTATTG TATTCTATTT TCTTTTGGTT ATTCAAATAT TTTTTGGTAA   3000

TTGGCTTTAG AATTTCAATA TTTgTTTCC   3029

(2) INFORMATION FOR SEQ ID NO: 40:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 3000 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CnCACAGnAC CTTTTAAAAG AGTATTCTAT TTTCTTAATT TATAAAAAAA TAAAATCAAG   60

GTAAGAACTA TTTAAAATAA ATCTTGTGAA TCTTTAGTAG TGAATGATTG TCTGTCCTAG   120

TAACTTAGAA CTTAGAAAGT TAGCAAAGCA AACTTTCCAT CCTTCTTCAT CTCATTACCA   180

AAATCCGCAT CCTCATCACC CTTTCCAATA GCAGCAGCAA TCGGATTTGT AGCCTCCCCA   240

GGCTTCTCTC CATCCTGCTC AGCCTCACCA GCAGCCTTAA CAATCGCACT TAATATCTGC   300

TCCCCACTAA CAGCACCAGC CGCCTTGCTA GCAGCCTCAC TGTCCCCAGC ATTAGCATTA   360

TCAACTTTCC CAAACAACTT CCCTGCCTTT TTATTATTCT CCCCTGCAGC AGCAGCAACT   420

TTCAGCTTTT CACTCCCCCC AGCAGCTTCA ACAATCTCCT TTATTCCCTT AGCAATCCCC   480

GTCACACTCG CCTCATCAGC AGCCTTCGCA GCACTATTAT CAGCCACAAC TTCTCCAATT   540

GCATCAGTAC CACTTGAAGC CCCCTCAGCT GTCTTTACAC AGCTTTTACC AGCTTATCCA   600

ACAACTCGCT AACTTCTTTA ATAGCCCCCT CAGCCTTCTC TTTCTCACCA CCACCACTCT   660

1009

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TCACAGCAAA CTTTCCATCC TTAGCCATCC CCCTCAAAGC AATAGCAGCA GCAATCTGAT    720

CATCCTTCTT CATCTCATGA TTAAACTCCG CACCCCCATC TTTATCCCCA ATAGCAGCAG    780

CAATCGGATT TTTAGCATCC TCAGGCTTCT TTCCCTCCTG ATCAGCCGCA CCAGCAGCCT    840

TAACAATCGC ACTTAATATC TGCTCCCCAC TAACAGCACT AACAGCACCA GCCGCCTTGC    900

TAGCAGCCTC ACTGTCCCCA GCAGCAGCAC CAGCCTTCCC AAACAACTTC CCTGCCTTTT    960

CATTGCTCTC CCCTTTAGCA GCAGCAACAG CTTTCAGCTT TTCACTACTC CCCCCAGCAG   1020

CTTCAACAAT CTCCTTTATC CCCTTAGCAA TCCCCGTCAC ACTCGCCTTA TCAGCAGCCT   1080

TCGCAGCATT ATTATTATCC ACAACTTTTC CAATTGCATC AGTACCATTT GAAGCCCCCT   1140

CAGCTGTCTT TACAGTTGTT ACCAGCTTAT CCAACAACTC GCTAACTTCT TTAATAGCCC   1200

CCTCAGCCTT CCCTTTCTCA CCACCACTCT TCACAGCAAA CTTTCCATCC TTAGCCATCC   1260

CCCTCAAAGC AATAGCAGCA GCAATCTGAT CATCCTTCTT CATCCCCTCC TTATTAAACT   1320

CCGCACCATC ATCCGCATTA CCCTTCCCAA TAGCAGCAGC AATCGGATTT TTAGCCTCCT   1380

CAGGCTTCTT TCCCTCCTGC TCAGCCGCAC CAGCAGCTGC AGCCGTAACA ATCGCACTTA   1440

ATATCTGCTC CCCACTAACA GCACTAACAG CACCAGCCGC CTTGCTAGCA GCCTCACTGT   1500

CCCCATTAGC AGCATCACCA GCTTTCCCAA ACAACTTCCC TGCCTTTTTA TTATTCTCCC   1560

TTGTAGCAGC AGCAACTTTC AGCTTTTCAC TCCCCCCAGC AGCTTCAACA ATCTCCTTTA   1620

TCCCCTTAGC AATCCCCGTC ACACTCTCCT TATCAGCAAC CTTCGCAGCA GCATCATTAG   1680

CCACAACTTC TCCAATTGCA TCAGTACCAC TTGAAGCCCC CTCAGCTGTC TTTACACAGC   1740

TTTTACCAGC TTATCCAACA ACTCGCTAGC TCCCTTAATA GCCCCCTCAG CCTTCCCTTT   1800

CTCATCACCA CTCTTCACAG CAAACTTTCC ATCCTTAGCC ATCCCCCTCA AAGCAATAGC   1860

AGCAGCAATC TGATCATCCT TCTTCATCTC ATGATCAAAC TCCGCACCAT TCTCCGCATC   1920

ACCCTTCCCA ATAGCAGCAG CAATCGGATT TTTAGCATCC CCAGGCTTCT TTCCCTCCTG   1980

ATCACCAGCA GCCGCACCAG CAGCCTTAAC AATCGCACTT AATATCTGCT CCCCACTAAC   2040

AGCACCAGCC GCCTTGCTAG CAGCCTCACT GTCCCCAGCA TTACCAGCAT CAACTTTCCC   2100

AAACAACTTC CCTGCCTTTT TATTATTCTC CCCTGTAGCA GCAGCAACTT TCAGCTTTTT   2160

ACTCCCCCCA GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCT TCACACTCTC   2220

CTTATCAGCA GCCTTCGCAG CAGCATCATC AGCCACAACT TCTCCAATTG CAGCAGTACC   2280

ACTTGAAGCC TCCTCAGCTG TCTTTACAGC TGTTACCAGC TTATCCAACA ACTCGCTAAC   2340

TTCCTTAATA GCCCCCTCAG CCTTCCCTTT CTCATTATTA TCCTTCTTCA CAGCAAACTT   2400

TCCATCCTTA GCCATCCCCC TCAAAGCAAT AGCAGCAGCA ATCTGATCAT CCTTCTTCAT   2460
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CTCATCCTTA AACTCCGCAC CATTCTCATT ACCCTTCCCA ATAGCAGCAG CAATCGGATT   2520

TTTAGCCTCT GCAGGCTTCT TTCCCTCCTG CTCAGCCGCA CCAGCAGCCG TAACAATCGC   2580

ACTTAATATC TGCTCCCCAC TAACAGCACT AACAGCACCA GCCGCCTTGC TAGCAGCCTC   2640

ACTGTCCCCA GCATGAGCAG CATCACCAAC CTTCCCAAAC AACTTCCCTG CCTTTTCATT   2700

GCCCTCTTTA GCAGCAGCAA CTTTCAGCTT TTCACTCCCC CCAGCAGCTT CAACAATCTC   2760

CTTTATCCCC TTAGCAATCC CCTTCACACT ATCCTTATCA GCAGCCTTCG CAGCATCAGC   2820

CACAACTTCT CCAATTGCAT CAGTACCACT TGAAGCCCCC TCAGCTGTCT TTACAGCTGT   2880

TAcCAGCTTA TCCAACAACT CGCTAGCTCC CTTAATAGCC CCCTCAGCCT TCCCTTTCTC   2940

ATCATCATTC TTCACAGCAA mCTTtCCATC CTTAGCCATC CCCCTCAAAG CAATAGCAGC   3000

(2) INFORMATION FOR SEQ ID NO: 41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2991 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAAAAAAC ATGAATTTAG ACTATCATTG AGGGCCTTAT TTAATGGAGA AAGAATTGTT   60

GAAGAAACTC ATTTGTACCC AATTAAAGAA GGAGATAAGT TTATTGGTAT TTTTTATGGC   120

TACAGAAAAC CAATAAAAAA GCCATTAATA AAGTATCAAA TAAACGGGGC TAGAAAAGCA   180

TATGCATTAG CAAGGGCATA TTATATGGAA TTTAGATTTA AAGCCGGAAG TGTTTTTTGC   240

TATTTTAAAG GGCTaTATCG ATTATTAGAT AAAAAAGAA CAAATAATCA TTACAACAAA   300

GTTTTATTTA GTATGTTTAC GGATTTAGAA CAACAAGTAT ATAAATTTTA TGGGAAAAAA   360

TACCCGGAAC AAGGACCGTT AATAAAATGG ATACTAAAAA ACCTAAAATA ATAACAATAG   420

CGTCAATCAA GGGCGGTGTT GGGAAAAGTA CGAGTTCAAT AATATTTGCG ACATTATTAG   480

CTCAAAAATA TAAAGTATTA TTAATAGACC TAGATACTCA AGCATCTACT ACCAGTTATT   540

TTTGTAAAAA ACTTGAAAAT CAAAAAATTG ATCTTGTCAA TAAAAACATA TACAGAGTAT   600

TaAAAGATAC ATTAGATGTA AATAATGcAA TTGTAAATAT TaAAGAGaAT TTAGaTTTAA   660

TACCAAGTTA CATAACTTTG CATAAATTTT CAAATGAATT TATACCCCAT CAAGAGTTGA   720

GATTAAAAGA TAGTTTAATC TTTTTAAAGC AAGATTATGA TTATATAGTA GTAGATACTA   780

ATCCTAGTTT AGATTTTACT TTATCAAACG CTTTAATAAC TAGCAATTGT GTAATAGTTC   840

1011

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CAATGACGGC AGAAAAATGG GCAATAGAAA GTTTAGATTT ATTAGAATTT CATATTGAAA    900

ATTTAAAAAT AAAAATACCA ATTTTTCTTC TTGTGACAAG GTTTAAAAAA AACAATACTC    960

ATAAAGAATT ATTAAAATAT GTTGAATCTA GGGAAAGATT TTTGGGATTT ATTCATGAAA   1020

GAGAAGATTT AAACAAAAAA ATTGCGGGCA ATAATGAATT CAATATGGAT AAAGACTATA   1080

TTAATGAATA TAAAGAAGCA TTATCAAAAT TTTTTGAGAT ATATTAAAAA ATTTATTATA   1140

AAAAAAATCC AGATTCTGGA CTTTTTTGAA ATAAAGGAGA TTTTTTATGA AAATAGAATT   1200

AAATAAAAGA ATTTTGGCAT CAGGGATAGA TCCCGATGGT AAAAAAGAAG TGATTACCAA   1260

TGAAGATAGA ATTGCTCATT ATAATGCTTT GAAAGATAGA TTAAAGGCTA ATTTTAGAAA   1320

AGAAATATAT CATAAATTGG ATAGCATCAA AATTTTGAAA GAAATAAAGG ATAATCAATA   1380

TTATAAAATT GATGGATATA AAAAATTTGA CTATTTTATA AAAGATTATA AAATAGCTAG   1440

AAGTCAAGCT TATAATTACT TAAAATtTAc AACTGCGTTG CAAGAAGGAA TTCTTAAAGA   1500

AGATTATTTA ATAGAAAATG GCATTCATAA TTCTCTTGAT TTAATAAAGG ATAAAGAAAG   1560

TCCAACATTA AAAAAGTCTA AACAAAATCC AATAAAACCT CTAAGATTTC AACTTAAAAA   1620

TCAAGAAAGT TATGATTTTT ATAAAAGCAA TGCTAAATTT ACGGGATTCT TGTTAGATAA   1680

ATTATTTATG GATAAAAAAG AAATAATTAA AATAATTATG AAAGAATATA AACAATTAAA   1740

GGGATAATAT GGAGGTTGTA TGAACAATTT AGCTAACAGA ACGTTTAACA TAGGAAATAT   1800

AAAAAACGAA TTTTTAGAAA TAGGATTTAG CGAAGAGGcA ATAGATTTTG TTTTTCTTCA   1860

TAATGATAAT TATAACTTTG AGTTTTTAAA AGAGAAATTG ATTAATTTAG AGAAGAATTT   1920

ACAAAAAGAT ATATCTAATT TAGATATCAA AATAAATAAT GTTAAAAACG AACTTAATGC   1980

TAAAATAGAT AGTGTAGAGA AGAATTTACA AAAAGATATA TCTAGTTTAG ATATCAAAAT   2040

AGATAGTGTA GAAAAGAATT TACAAAAGA  TATATCTAGT TTAAACACCA AAATAGATAG   2100

TGTAGAAAAG AATTTACAAA AAGATATATC TAGTTTAAAC ACCAAAATAG ATAGCGTAGA   2160

AAAGAGTTTG CAAAAAGATA TATCTAATTT AAACACCAAA ATAGATAGTG TAGAAAAGAG   2220

TTTGAATCAA AAACTTAGCA TGGGTAACAG ACTAGTACAT TTTATGATAA TAACAGCAGC   2280

AATTCTAGGT CCAATTTTAA ATGCCCTATT TATGAGGTAT TTACAATACA TCAAATAATG   2340

ATGTATTGTA TAATTTGATT TTTAAAATGG TACATTATAA TATTGATGAA GAGTATTATT   2400

AATTAACACT TAATTTTTGC TTTTTCATAA AGTAGAACTT ATTTAAATTT TTTAACAAGA   2460

TAACTTAAAT AAGTTCTTTT ATTTTAACAA ATACAAATTG ATTTTAATTC TAAATTGGAC   2520

TATACTCAAT TATTGAAAAG CTTTTTAAAA TTATTTTAAT AAGTGAATTC GGTTAAACCC   2580

TAGCTTTATT AAGTTCTTTA ACAAGAGAAT TTAATAAAGC TTTTATTAAT TATAATAATT   2640
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TCTGTAAAAA GTTGGCAAAA AACAATTTAT AATATTATTA TAAATATTAT AGGAGGGATA   2700

TGTTATTATA AATCCGATTT AGTTTGGGCT TAACTAAGTT CTTTTGTTTG AGAATATAGT   2760

TAAGCTCTTT TTTTTATAAA AATTGTTATA AAAAGTTGGT AAAAATAGTT TTTGTTATAT   2820

ATATGTATGT GAATAGCTAA AAAAGTGTAT TGCTATCAAA ACAATCCAAT TAAGTTGGGT   2880

TTAGCTAAGT TCTTAGACAA GAGAATTTAA ATAAGCCCaA CTATTTTTTT TGTAAAGATT   2940

TTTGTAAAAA AgTTGGCAAA AATAGTTTTT GCTATATACn TATATTTATG n   2991

(2) INFORMATION FOR SEQ ID NO: 42:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2988 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTATTTGAAA ATTGCGAGCA TAATATGTGT TTTTTTATTT TAGCACAAGT TTTTTAGACT   60

TTCTAAAAAA GTTAAAAAAA AAGAAGATGC TGAGTAATTT GTATAGTTCT TTTAAGATTT   120

TCATTTAAGT AATAAATTAT ATTATCTTGA TATACTTCTA ATATTTACCC ATCAATAAAG   180

CTAGTGTGGC TTAACAAATA AAAACCAATA AATATTTAAA AAATGATTAA TTTAGAATAT   240

AATTTCTATA GCTAAAGCAA AAAATAAATA TAAATTTGGA CTAGTTTTAT TACATAAAAA   300

GATAAAATTA GTCATGCTTG TTGCAATAGA GCCTACTATC TATCCCGCGA GGTATATTTA   360

TTTATATTGC TTTTTAGTTT TTGTAAAGTG ACTTTTAATT ATTAAAATCT AAGGAGAAGA   420

GATTTATGAA CAAAAAATTT TCTATTTCAT TATTATCTAC AATATTAGCC TTCTTGTTAG   480

TATTAGGTTG TGATTTGTCA AGCAATAATG CTGAAAACAA AATGGATGAT ATTTTTAATT   540

TAGAAAAGAA ATACATGGAT AATTCAAATT ATAAATGTTT AAGTAAAAAT GAGGCTATAG   600

TTAAAAATTC TAAAATTAAA TTAGGTGTAA ATAATACTAG AAGTCGTTCT TATTCTTCTA   660

GAGAGACTAA TGTTTCGGAT TCCTATAATA AAACCTATTC ATATTGCAAA AGCAACTGAT   720

TAATTTTATT ACAAAAAAAC AAGAGAATGC TCAACCCATA ATTAGGTGAC AATTAATTGA   780

ATATATGCAG GGATTATTAA AAGTTAGCTT CTGTGACATT ATACACTTGA ATATAATATT   840

ATAAAATAAT AGAATATATG GGTGTTAATA AAGCTTATAA GCATAGAATA TATCATATAA   900

AGAAGAATTT CTATCCCCTT AAAGGAAGTT GATAGTTTAG CTCTTTGTAA TGTCCAACTT   960

GACTTAGACT CTGCGTATAA TGATTTTTTT AGAAAAATTT AAAAGGGAAA TAGAACACAA   1020

1013

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GGATTTCCTA AATATAAAAG TAAGAAAAAT AGGGAAACTT ATAGAACTAA TAATCAAAAA    1080

AACTCAATAG GAATAAAAAA TGGTTATATA AAGCTACCTA AAATAGAGTT TATAAAGTTA    1140

TGTCTATAAA TATTATATTT CAATAACAGT TGAGTGCTTA GATACTAAAA ATAATAATGA    1200

AACTAAAGGT GATAAAAAAG AGGCAGTTGG TATTGATATG AGCATGAAAC ATTTTTTAGT    1260

AAGTAGTGAA GGTGAGAAGA TTAATCATCC TAAATATTTA TTAAAAAATG AAAATAAACT    1320

TAAAAAATAC CAAAGAAAAC TATCAAAAAA GCAAAAGGT TCTATTAATA GAGATAAGTC     1380

TTAAGGTTTA GACTTGCATT TATATCTCCA TCATGCAAAG TTGTTACAAC TACTGAAAGC    1440

CCACCTAGTA TCACTTAATT TTAGAGCCAT ATTTTTAATA TGACAACTAC TACATACATA    1500

TAAATCAAAA TGGTATGGAT CTGCTTTGTA TAAAGTAGAT AGATATTTTC CATCAAGTAA    1560

ACTATGTAAA TTGTCTTGCA AACTCAGACC ATCCTAAATC ATTAATACTT TTTCCAAACA    1620

TTCCTTTTCG CATGCCTTTT TTCATTCTTA GAATTCGAAC TGTAATCAGA CCTTTATATT    1680

CTTTATCAAT TATCATATTT TAGATTTAAA TTGTATATAG CAAAAAGGTC CTATATGGGC    1740

TATTCCGTTT GCAGTAAATA AATAGGGATT GGAATTAAAT CCCTAACCTA ATTGAATAAT    1800

ATCATACTTT CTTCAAGAGG ATTCCCTTCG GCCACTTTTT TTCTTCGTTC TTCCATTACT    1860

TTTTTATATT TTTCAGCTTG TTCTCTTCTT TTTTTATTTA ATTCTGTCGA TTCTCTTTTC    1920

TCTTTTTATA ATTTTTCTTG AACTACTAGT GGCTTAACTG TTTAGATTTG GGATCGTCCT    1980

AGTTATAATT TTGGTACTTC TAATTTTTCT GCTACCACCT TTAATTCTGC CTCTAGATTT    2040

GCTCAAATTT TAGGGATTGA TTCTAATTCA TCTCCTTTTA AAGATTTTTT TCTTCTACTT    2100

TCTTTCCCTT ATGTGCTTTT AAATCAAATC TTTTTGAATT ATCCATAGCT TCTGTTGCTT    2160

TTCATATACT GTTGTATAAT CTAGTGTCAT TTTATTTGGA TCCATTTTAT TTTTAGATGA    2220

TAACTTTTCT AACTTTTTTT ATTATCTTTA TCTTCTTTTT TTAAATCACA CGAAAATAGT    2280

AAAAATAATA GCAAGTAATG GCTAGGCATA TACTTATCTA ATTTAGAGAT TAGCTCCTAT    2340

ATTCAAGCGG CTATTATCCT TATTCTTCTG GCATAGAAGT TGAAAATTTA AATTTTAATA    2400

AATTGTATTT TTATTTTAAT GAGAATAAGC AGAAACATTC CATTCTTAAT TGAATTCATT    2460

AGAAAGTTTC CTTCTATTGC TAATATCATT AATATAATAA AATAATTATC AAAAACATTA    2520

GCAAATCCCC CTTTATCTCT ATGATACTCC TTCACATCTA TATGATTTCT ATCTTTACTT    2580

TCTACATTAG GCTGATTATC TCTACCATAT TTAATATAGC TAAGCGGCTT TTTAACTTTA    2640

CCCATATTTT TCAGTTTGAA TAAAAACCTT TTAACATACT CTTCTATTTG GGATACATCT    2700

CCTTTTCAAT AAAAATTAAA ATGCGCTGAT TTTAATACAT TTACGAAAAA AGTTAATGTA    2760

TCGAGTTTTT CATTACTAAA TCTAAGATTG CTTTTCTAAC TCAGTTTTAA ATTAATACTT    2820
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TCATAAGCTT TACAAGCTTT AGTCACTCCT CATATAAAAT CCAAAATTCA ATTGTTTTAT   2880

ATAAGTAAGT ATCAAGTAAA TTTAAATTGG ATAGTAAAAT ATTAAATAGG GGAAAAAACA   2940

AGCTTAATAT TGAGTGATAA ATAAATTTTT CTCTTATTAA ATAGTATA   2988

(2) INFORMATION FOR SEQ ID NO: 43:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 2970 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGAGTTTTTT CGTTCTTTAA AGTACTTGTT GATTTCTGG TAACATTCTT TTTTAGGATA   60

CTTTAGCTTA TAGTAAATTT CAGTtCCACA ATTTACACCC ATGTGTTGGT AGTAATTCGT   120

TGTGACTTTT AATACTTTTT CTAATTTATA AAGATAATTT TgCaTTGTTC TCAGTGTAGT   180

GGGAGCCAAA CCATTTCTTT TTAGATTTTT ATTATAGTAA TAGAGTATGT TTTGTTGTGT   240

ATATTTCTTA TCTTTTTTGT TTAGAAAATC TACTGTTGAT GTAAGATATA TTAACTTGTG   300

TTGGTGTTTG TTGTGGCAAG TGGGATTTTT TGTGGTGATT AAAAAATCTT TCATTTTTA   360

CTCCTTATTT TGTTATTAAC AATTACTATT ATAATGCAAA ATTTTGATTT AAAAGTAAAT   420

ACTTTTCTAA AAAAATATTA AATTTTAATT ATTAATCTTA TTAATTAAAT ACACTTTTTG   480

TAATTTGGTA AAAAGATTTA TTGATTTTAA TCACAAATTA GACTATACTG CAAATAGCGT   540

AGGAAAATAT CTTCATATTT TTACCTACCT TATTTTGTAG TTTTCTAAAA TCATAGTGGG   600

AACTTGGCGA AATTCTTTTT AAAGGGAATT TGGTTAAGTC CCACTTCTTT TGTGTAAAAT   660

TTTTTGTAAA AAAGTTGGCA AAAATAGTTT TTGCTATATA ATTATTTATT ACAAAATAAG   720

GAGGAAAAAG ATGGAAAATC TTTCAAACAA TAATAATCCA CAAGAAAATA TTCAAGGAGA   780

AATTAAATTC AGAAAGATA TGAGCACCCT AATCAGAAAC TTGCCGCGTA TTGACAAAAG   840

TCTTAAAGGG TATGGGTATA AGTATCAAGA TTTCAATGAC ATAGTAGAAG TAATTTATAG   900

TGTTATTGAT AAGCATAATT TGGATCTTTT TTTTACGCAA GCCCCAATTT CTGTAGAGGG   960

GCAATATGGC ATAGTTGATT ATATTAGGAC TACATTCTAC AGTACAAGCA CTGTGTACAA   1020

ATACTCATTT GATACGCGAA TTCATACAGA TAAATTACAA TGGAACAGTG AAAATGGGTC   1080

TAAAAATATG AATACGATGC CACAATTTGT TGGATCAGCT ATTACTTATT TCAAAAGGTA   1140

CGCTTTAGTA GGGCATCTTT GCATAAGAAG CGAAATGGAT ACTGATGCAG CACCTATTTA   1200

1015

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CAATAATTAT GAAAACAGAA ATTCTATGCC TAGCAAACAA TCTAGTGTTA ATCAAAAGCA     1260

AGAACAAAAA AGAGAGCAAA AACAAGAGAT TAATCAAAAT CAAAAAAATA ACACTATTCA     1320

AAACCAGAAA AGAGACATTA AGCAAGAACA AAAAAAAGAT AGGTTTTATT ATTACGGTGT     1380

TTTTAAAGAA GCGTTGTCTA ATATAAAAGA TTGGGTAAAT AGCCCTACAA TAAAAGATAA     1440

TATAAACTCA ATTATTCAAA AAATAAGCTT TATTCAGAAT ATAGACCCCA ATAATGTTGA     1500

TGATATCAAG AAAATTGAAT CTGATTTAAT CTCGTATTTT GAGAAAAATA GTGATTTTAA     1560

AAGTATAAAC TATTGGGCGG AGATTATAAA AAACTATTTC AAGAAAAATA ATAGATTAAA     1620

GGATTTACAA GATTTTGAAA AGTTTGTGTC GTTAAGAGG ACTGCTTATG GCCCTAGTCC     1680

ATTAATATTC TTTAGTGTCT TAAAAGAATA TGAACGGTTT GATTGCATAT TTGCAGCATA     1740

GCGAATTCTT ATATGGTGAA GCCCCCACAT GGGGGCTGCG ATATTATTGC TGAGCTTGGC     1800

AGGTACTACT TGCACTAGTT GCAAAACTAT CTATACCGCC ACCAAGAGCC CCCTTAACCA     1860

CCTCTTTGAA GGTGCTTTTT TGTTGTTCAG AATTATCCCC AGTACACTTA TCAAGTTCAC     1920

TCTTTATATG ATTAAGTGCA CCTTTTATTT TGTCTTCGTC ATATCCTAAA AATTTATCAA     1980

ATTCTCCAGC ACCAGTTAAA GCGGTTTTTA ACCAGTCAAG ATGTGTTTTT TGGTCTTCAG     2040

ATAGCTTTTC TCTAAGCAGG TCTTCTTTAG ATTTTGGTTT TTCTTGTGTT GCTTCTTTTT     2100

GGGTTAAATC ACGTTTTTGT CTACTTTTTG TTTGGCTAGT ATTAGTATCA TTAGAATTAC     2160

AGCTGTTTAG CATTAGTAAA AATAAACAAA ATAATATGTT GATAATTTTC ATTrTTATTC     2220

CTTTTTTTAT TATTAATATT CACTTAATCA ATTATTAATA CTAAATATTG GATAAACAAT     2280

TATTATTTGA ATTGATATTC TTTAAGTGAG GTAGTAGCTA TTTAGAAATG AAAGCAAATA     2340

TTAGCCCGGC TATCATTGTT ATAGACATTG CTCCCATAAT TCCTAATACC CATTTAAGCA     2400

TTTCTGAAAG AGACATTAAA TTCTTTTCCA CATTGTCTAT TTTAGCAGTA AGTTCATTTT     2460

TAACACTATC TATTTTAAA TTTAAATTCT TTTCTACAGT ATCTATCTTA GTATCTAAAC     2520

TATCTATTTT TAGATTTAAA TTCTTTTCCA CATTGTCAAT CTTAGTATTA AGTTCGCTTT     2580

TAACAGCATC AATCTTAACA TTTAAATTCT TTTCTACAGT ATCTATTTTA GAAATAAGAT     2640

TATCAAATTT TATATCAAAT TGTTTTTCTA AATTTTCTAA ATCTCTATAT GTTAGTTCAT     2700

TGTGATAATA TCTTTTAGAT AAATCTTGTG CTATTAGTTG TTCCATGCCC AGTCTAATAA     2760

ATTCTTTATA TATTTGTTCT TGAGTTACAC CTGCAATATT TGTTGACACT GTTTCCATAA     2820

AATTTTCCCT TATGGTCATA TTATACACTA TTTTAGATTA ATTGGCTTTA GAGATTTTTA     2880

TATGTAAAAT AGAATTTCTT GCAAGAAAAA CCTTTTTGTA ATTTACATTT TTAATTGGGA     2940

ATATTTATTA TAGACTTTTT CCGCTATTGG                                     2970
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(2) INFORMATION FOR SEQ ID NO: 44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2942 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

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AGAATAGCTT GAAGTAAGGA TAAATGAAGT AGAAAATTTT GCCTGCTTAG TGCAAATTTG      60

TCTATTCCTA ATAGCAATAA CACTTCTGAA TGGAGTTTTG TTACTAAAAG TTCTTCTTCT     120

CCCGCAACTT GTGCTTGTAA GCTTTCTTGT TCACTCATTT TCACTTACCT TATACTTTTA     180

ACTTTGCTTT ATGTTAACTT GCAAAATAGT TTTTCTAGTA GCAAGTAGAC CGCCTAAAAC     240

AAAATCAATG TATGAATGAG CTACATCGGT TGAGTCTTTA TCAACTTGTT CATTCGGTGT     300

AGGTAGCATA TACTTACTAG GTTTAAATTT AATAAGTTCT GAATTGAGTG GATAAATGAG     360

TATTTTATGT TTTAGCAAGT TTGAAGTTTC AATGTAAACA TCTTCTCTAT TATTAATAGC     420

CTTAATAGTT TGAATTAAAA CATCTTCCCA TTTTTCACAA CTACTTGCTG CACCCTGTGC     480

TGCTGCGTAT GGTTTTACTA GTTTAAGTGA CGTTGCTGGG TCAACTATTA CCATCATCGG     540

TGTGGAAAAT TCGTCGCCCA GTTCCAACTT TGAAAGTCCA GCCTCAATTT TTTCAAATAT     600

TTTATCCATT TTATCTTTAT CACCACTAGC AACCTCTTCT TTTATCTGCT CGGGCATATT     660

AAGCAGCCCA TACATATTTG GAAGCAGGCG TTTTTGATTT TTTCCATCTT TTTGAATCGA     720

AACAGTTCCT GTTAGTACAA AGTGATTAAT AAGTTTAATA ATTTCACTAC TTGCAAGCTT     780

ATACGCTTGA GCAAAAGGAA GTAAATTATT ATTAATGTCC CCAATATATG AATCTGAAGT     840

ATAAAATTTC TCAGAAGTCT GCTTTAAATG TCTGAATTTA TACTGTAATT TCAAATAATT     900

AAGTCTTACC ACTTCAGAAC TAAATCCAAT AGTTGAGATA GTATTAACCT CATTGGCAAT     960

TGTTGTAGGA TTAGCATTTA AAAACGCGTC CCATTTTACG GTTTTTTGAT ATCCCATTTG    1020

TAGATCAACA TCTTCAATTT GATCGGGCGA AAACCATTTA TACATAATAG GATCTTTAAC    1080

TTCTCCTATG ATATTTGCCA CAGCTTTTGC ATAATAATTT TCATCAAATA ATTCCATATT    1140

AAATCCTCCT AAATATTATT AATTTCTACT CATAGCTTTA TTCCCAAATA CAGCTACTTT    1200

TACTAAATAA ACCTCATTGC TAATTTGTTT CGCATCAGTC AATGCTGTTG CATTAATAGT    1260

TGCTTTATTT GGTGCTCCAG TCACCTTTTC AAGAGCACCG TCTTTATTAA AAACAAGTTT    1320

GTCTTTTACT TTAACCGTAG AATCTTTTGC CACTAAATAT CCCTCAAAAT TATTGGTAAT    1380
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TGGCACAATA GTAGCTGTTT TACTAAACTC ATCTATGTCA ATGCATATTC CATATAAGTC      1440

TTCACCTCCA CCAGCCTCAA CATGTGGCTC ATAGTGACTT TGATTATCTT GAGCCTCTTG      1500

AATAACTCTT TTTACTCCAC GCTTGTACGG ATACCCCAAA AATGGATGAT TTTCCAATTT      1560

ATCAAACTTA CTAGTTCTAG TGCCTCCAGA AGCAAAAAAT TtCaCATTTT TGTCTCTAAA      1620

TTCATTAGAA TTGCTAAGCA AACTAGCGTC ATGTTGGGGA TTTTtCATAA ACTTTTCCAG      1680

TTTACTTCTT TtCTCTkGAT ACTCTTTTAC TAATTGCGTT GTATCTCCCA TTTATTTACC      1740

TCCTTTTATT CGCCCAAAGT TTAACCACCA TCAGGTATTA CTATCTTCTC AAGGCCTCTA      1800

TTTCCAAAAA TTGCAACTTT TATCAAATTA ATAGAATACT CTTGCCTAGG ATATCTATTT      1860

TGATCTtGAT TTCCAtCTTC GGGTGCAAAA TTGATtGTAA ATGAATCAGA TAGAGCATAT      1920

ATGTTAATTA CGGTTGGTGG CCCACCTCCA GCCTTGATAA TAACACCGTT ATTATTTATG      1980

TCTAGGATTT CTCCTATTTT TATACTTGGA TTCCTTGTGA CAAGGTACCC TTCAAAATTG      2040

TTAGTAATTG GCAATACATA CGCGGTACAA CTAAACTCAC ATACATCTAC ACATATCCCA      2100

TACATATCAG TATCAGCTCC AACTTCyACA TATATAGAGT CTCTTTTGG AACAAGTTTA       2160

ACCCCACGCT TGTATGGAAA ACTATTTGCT GGGTCGTAAA GGTATTCCTC TATTTTGTCT      2220

GTATAACTTG AACATGCAAA TGAATATGCA TCAACTCGCT CATTCTTAGA TTTAAAACAA      2280

CTACTCAAAC CGCCAAAAAC CTTATTTTCA ATTGAACTCA TAGATTTTAC ATATTTCTTG      2340

AATTTCAAAA GGATATCATC AAGCTCGTTA ATTGCCTCCA AATAGGGATC TTCCCCTTGT      2400

GCATCCTCAG CTTGTCTTGC TTGCCGTTTA GCTCTAGGAG CAGCGGAAAC TTGTGCCCCT      2460

AAATCTACCT GTGGGTCCTC AACAGCCTCA AGATTTTCTA CTTGCATGTT GCCTTTTAAA      2520

GCCATAATTT ATTACCCTTT TATTGCTCTA TTCCCAAATA CACTAGCAAG CACTATAAAT      2580

AAATCTTCAG TTAATTTGTG TGCCTTTGAA AGTGCTATTG CATTAACAGA TTTTTGAGCC      2640

CCAGTGACCT TTTCAAGTTC CCCATGTTGG TTAAAATTTA ATTTATCTCC TGGATTTACA      2700

CCATTTTGTC CTTCTTTCTT AAGCGTTAAA TACCCAGTAA AGTTATTTGT AATTGGTATA      2760

ACAGTTGCCA TACCGCTAAA CTCATCTATA TCGGAACACA CTCCATATAA ATCGTCTCCA      2820

CCACCAGCCT CAACTTCTAG TTCGGTTGTT CCATCTCCAA AACTAAGCTT AACACCCCGT      2880

TTATACGGAT ACCCTTTAGC AGGGTAATTC TCTATTTTGT CTTTACTGCT AGTGCAAACC      2940

CC                                                                     2942
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(2) INFORMATION FOR SEQ ID NO: 45:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2892 base pairs
            (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

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GGGTCTATAA TGTCATTTAT TATTTCCTCA GTGCTTTTTC CAGTTTTTAT TCCGTATTCT        60

TGCGCTGCTT TATAAGAGCT ATACATTTGA CTTTTTTGTT CTTGCGTTGC TTGTTCGGTT       120

TCATAAAGTT TATTTATTGA CTTTTTTAAA TCTTCACTAA GATTATCATA AAAATTTGAA       180

ATTTCATTAG TATGCATATT AATTATAGAT AGTATATAAA TAAACAATAT TTTGAGCAAT       240

AGTTTTTGGC ATTTTTTAAA TGAAAGTTTT GATAGAAAAC ATTTCTATAT TCATAACAAT       300

GAAATCTACA AAAAAATAAC AGCCAGTGAA CTTTTCTACT AGCTGTTACT TTGTATACGC       360

AAATTTAGTT ACACCTAAAA GCATCCAATA TAATTACTGA CTGTCACTGA TGTATCCTTT       420

AATTTCTTCA AATTTAGAAC TATCTTTAAG ATATTTTTTA ACTTCTTCTA ATTTTGATTT       480

TAATTTTTCT AAATCTTCTT TAATTTCGCT AACATTTACA CTTTCTTTTA ACTTAGGCTC       540

TTCGTAACCA GTATATGGTT TATTGCCTTC ATTTAATTTA GTTCTTAGCG CGTCCCTAGC       600

ATCACTCAAT TCTTTCAATA ATTTTCCTAA TCCTTCGTCT TCTGATTCCT CTTCTAACCC       660

CTCCCAAGTT TCGCGTATAG AATTATTGCC ATTGGTAAAA TCATCATACA CAGGCCCAGT       720

AATTCTATCT ATAACGCCTT GTGGGCCTAC AGTCGTTTGC CATTTTATAA CATCAATATT       780

TTCATTGAtC TCATCTATTT TAGCTATAAG TGTTTTAATT TGGTTATCAA CTTGCCTTTT       840

TTCTTCCTCT TCTTGTTGTC GTTTTTGTTG TTCTGCCTCT TCTCTTTCTC TTTTTTCTTT       900

TTCTGCTTTA GCTTTTCTTT GTTGCTCTTC TTGATGTCTT TTTTGTTCTT TTTGTTGTTC       960

TTCTTCTTTA GCTTTAGCTA ATTCTTGTTT GTTTTGTTCG TCTATTATTT CTTTTTCTTT      1020

AATGTTTTCT TCTGTATTCT CTTGTTTTTC TTTATTTTCT TCAACTTTAG CTTCAGCTTC      1080

TTCTACTTTT TTTTCTTGTT GACCATCACT TTGTTCTATT GCTTTTAATA CTAATGCATT      1140

ATTGTGAATA TTTTCCGGCA ATACTGGTGG CGGATTTATT CCACTGCCAT TAGGATCATC      1200

GCCCTGCATT AATTCTTCTT TTTCTTCTTC TTGTAATTTT TTTGCTACTT CATCTACTTT      1260

TGTACCACTT GAAGCAATTT TATCCTTTAC TGGATCTAAA ATCTTATTTA CAAATCCTTT      1320

AATTTTCCCT TCTGAATTTT GTTTTATATC TTTACCAGTT GCAAAATTCT TGCAAGAAAT      1380

TATCAGCGCA AAAACAGCAC AAATAATCAA TGTTTTTTTA TTCATAATTA TTCTCTCCTA      1440

TATTTCTAAA TTCTATTTTA AATTTTTTTT AAGCACTTCT AGTGGTATTG CATATTCAGC      1500

TGTTTTATCT CCCCCCACAC CGTTATTAAT TTTATCTCCT AAAAACGCAA TATGTTCAGC      1560
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1019

ACCATTAATA CTTTCTATTT TTGTTATGAT CTCTTTGTTT TGGATACCAT TTGCACTACT   1620

TTGTTCGTAC TTATATCCAT AATACAAACT AGTTTTAAAT GATCCGCCTT TAGTCATTGC   1680

TTTTATAAAG TTATTAACTT CTGATTCTTT TAATGAAAAG AATGTAGCCG AATGTCCCCC   1740

AGCGTTTAAA CCCGTATCAA TACCATTTTC TTCTTTTCTT ACAACTAAAT CTCCTAGGTC   1800

TGTCCAGTTA CTATTATTAT CTTTATTTTT AATTTTTACA GTAAATTTAG AGAATTCTAT   1860

TTTTTTAAGT TTTAACTCAC CATTACTTTG CTCATCATAT AAAGTATGGT TTATCTCACC   1920

ACTACTTTGC TCATCATATG AAGTATGAAT TTTGCAAGCA CCTATAAGTA TAAAAACAGC   1980

ACAAACAATA AACATTTTCA TTTTCTTATT CATAAATTTC TCCATAAGTC CTAATCATAC   2040

CACAACAGCT AATAATTGCA ATATTTCAAA GATTTAAATA TATAATTTTG TTACATTCAG   2100

CTATTACATA TTAACAAAAC TCAAATGTAA TTTTAACCAA CTCCCAAAAA TCTCTCCATT   2160

GCAAATGCCC GGCTCATTAC AAAAGACTAC AAAACACATA CAAATTAAAT TTCAAAGTCT   2220

TTGCTATATA TCACTTAAAG TATCATGTCT TTCTTAAGTC CACCCCTTAA AAATTGCCTC   2280

TTCTGTTTAT CACAGCCACT CCACAACCCA AATTTCGCAT GCAATGAGAA CACCATAAAT   2340

TTGACTAAAA TTTTAGGGTT TTGATAAAAT ATAAATTACA TTTTTATTAA ATTTTTATTA   2400

CTTTTACTTA ATTTAAAAGT AACACTTCAA AGGAGAGGAT TTTATGGATA CTAATAATTA   2460

TTTTAATTTA AATAATTTCG ATACAGATTT GATGCACAAA TTCTTAAAAG ACTATCAAAA   2520

TGTATTAAAT GAAAACAAAA TTCTTAAAAA TTCACTAAAA ATTTCTTCTA AGCCTACTAA   2580

AAAAGCTTCA AAACCAACTC CAAAGTTTTA TTTGAATCAA AAAATTATCA AAATAATTGA   2640

AAAATGTGTT AAAACATTAA AATAAATTGA CCCAATTTCT GGTTGGTTTT TAAATCTACT   2700

GGCAATAAGT GGCTGCAGAG GTGCCGAGCT GCAAAAGTA AAAATGCAAG ATATTACTCC   2760

CTTTTTAAGC AAAACTGGAG AAACTTTTTA CAATATAAAA GTAAATGTAG CTAAAAAAAG   2820

AAATGTCACT TGCATTAGAG AAATTGTCAT AAAATCTGTA GAATTTGATG CTATTCAAAA   2880

AGCTCACGAA AA   2892

(2) INFORMATION FOR SEQ ID NO: 46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2849 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCTAGAAAAG CATATGCATT AGCAAGGGCA TATTATATGG AATTTAGATT TAAAGCCGGA   60

1020

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AGTGTTTTTT GCTATTTTAA AGGGCTATAT CGTTTATTGG ATAAAAAAG AACAAATAAT      120

CATTACAACA AAGTTTTATT TAGTATGTTT ACGGATTTAG AACAACAAGT ATATAAATTT     180

TATGGGAAAA AATACCCGGA ACAAGGACCG TTAATAAAAT GGATAATAAA AAACCTAAAA     240

TAATAACAAT AGCGTCAtTA AGGGCGGTGT TGGCAAAgCA CAAGTGCAAT TATATTTACA     300

ACTCTATTGT CTCAaGATtG GAAAGTGCTT TtAATTGATA TGGATACACA GGCATCAGTA     360

ACTAGTTATT TTTACAAAAA AATAATAGAA GATAATTTTA ATTTATTGGA AAAAAATATA     420

TATGAAGTTT TGAAGGGGAA TGTATTAATT GATAATTCAG TTATAAATAT TAGTAATAAT     480

TTAGACTTGA TACCTAGTTA TATAAGTTTA CACAAATTTA ATAAAGAGGC TATAACATTT     540

AAGGAAATTA AACTTCAAAA ACAGCTATTA AATTTACAAT CCAATTATGA TTACATAATA     600

ATTGATACAA ATCCCAGCCT AGATTATACG CTAACCAATG CTTTAGTATG TAGTGATTAT     660

ATAATAGTTC CAATAACAGC AGAGAAATGG GCTGTTGAAA GTTTAGAACT TTTAAAGTTC     720

TCAATTAGTG ATTTAGCCAT TGATATTCCA ATTTTTTTAA TAATAACTAG ATTTAAAAAA     780

AATAATACCC ATAAGGCACT ATTTAGTTCG CTTAAAGACA ATAAGAATTT TTTGGGGTTA     840

ATTTATGAAA GAGAAGATTT AAATAAAAAG ATAGCAAAAA ATGATCTATT TAATTTAAAT     900

AGAGATTATA TGCTAGAGTA CAAAAATATA TTAAGTAAAT TTATAACAAT AATCATGTCC     960

AGGTAACTGG ACATGATTGC CATTTTAAAT GAAAGGAGTC CATATATGGA GATAATATTG    1020

AACAAAAGAA ACCTAGAAGT GCTAAATGAA GCCGAAGAAC ATTACAAGAA GTTAAaGCAA    1080

AGATTAAAAT CTAGTTTTCA ACAAGAAATT TATTATAAGA TGGAAGTTAT TAAGATATTA    1140

AAAGAAATAA AAGATAACGA ATATTATAAA TTAGATGGAT ACAGAACATT TGAAGATTTT    1200

ATCAAAGATT ATCATTTAGC AAGGAGTCAA GCATATGACT ATTTGAAAAT AGCAAATGCA    1260

ATTAAAGATG GCATTTTAGA AGAAGCTTAT GTAATAGAAA ATGGTGTTAC AAAAACTCTT    1320

GAGTTCTTAA GAAAATCGCC AAATGTTTTG AAAAAATCTA AACAAAATCC AATAAAACCC    1380

TTAAGATTTC AACTTAAGAG TCAAGAAAGT TACGACTTTT ATAAAAGTAA TGCTAAATTT    1440

ACTGGATATC TTTTAGACAA ATTATTTAAT AATGAAAAGG AAATGATTAA AAAAATTATG    1500

AAGGAATATA AACAACTGAa AGGATaGTAA GAAGTTTTAT GACTAATTTA GCGTACAGAA    1560

CATATAACAT AGAAAGCATA AAAAATGAAT TTTTAAACAT AGGGTTTAGT GAGGAGGCAA    1620

TAGATTTTGT TTTTCTTCAT AATGATAATT TCAATTTTGA ATTTTTAArA GAGAAAATAA    1680

TCGATTTAGA AAAGAATTTG AGAAAGATA TATCTAATTT AGATATAAAA ATAGATACTG     1740

TAGAAAAAAG TTTAAATCTA AAAATArATA CTATAGAAAA AAGTTTAAAT CTAAAAATAG    1800
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ATTTTGTAGA AAAGAGTTTA AATGCCAAAA TAGATAGTTT AGATACCAAG ATAAATAATG    1860

TAGAAAAAAC TTTACAAAAA GATATATCCA GTTTAGATAC TAAAATAGAT AGTGTAAAAA    1920

ACGAACTTAA TTCTAAAATA GATAGTATAG AAAAAACCTT GCAAAAGGAT ATATCTAGTC    1980

TAGATAATAA AATAGATGTT TTAAAAAATG AACTTAATGC AAGCAATAGA ACAATACAAG    2040

TAATTCTAAT AATGGGAATA ACACTtGCTC CAATTATCTA TTCTATATTT AATAAGTATT    2100

TCTTTAATTG AGAATGATTA AAATTTTTTA AAATATTAAG GGAGTATATA GCGTATTTTT    2160

TAAATAGAAT ACTATAATCT TGATTTAAAT TCTTTAAAgA AACATTTTAT TTTTACTTTC    2220

TTTTAAATTT AGAACTTATT TGAATTTTTT AACAAGAAAA TCTAAATAAG TTCTTTTATT    2280

TTAACAAATA CAAATTGATT TTAATTCTAA ATTAAACTAT ATTCAATTGT TGAAAAGCGT    2340

TTATTTATTA TAATAATTTC TGTAAAAAGC CTGACAAAAA TAGTTTTTGT TATATATATG    2400

TATGTGTATA GCTAAATAAG TATATTGCTA TCAAAAAAAT CCAATTAAGT TGGGTTTAGC    2460

TAAGTTCTCT AACAAGAGAA TTTAAATAAG CCCAACTAAT TTTTTGTAAA ATTTTTTGTA    2520

AAAAAGTTGG CAAAAATAGT TTTTGCTATA TACTTATATT TATTACTATA AAAGGAGTAA    2580

AAAGATGGAA AATCTTTCAA ACAATAATAA TCCACAAGAA AATATTCAAG GAGAGCTCAA    2640

AATGATAAGT ATTAATCAAC AAAGTTTTAC TGGTTGTGAA ATATTTGAGG AAAAATCTTC    2700

TCCCATTrAA GAAAAAAGTA AATTAAGTAA GATAGGCAAG AAATTGCCAG GaATAAGTAG    2760

TCAAGAATGT TTTAGATTTA ATCGCAATAT TGATTTTAGT GTGCAAAGAA ACAAGTTAGA    2820

TAAATACGGT GCTAGTGAAG TAGGCAATA                                      2849
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(2) INFORMATION FOR SEQ ID NO: 47:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2682 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

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AGTTGCGTAT CTTGACATAA AAAGTGAATT TGATACTGAT GCAGCACCTA TTTACAATAA     60

TCACGAAAAC GAAAATTCTA TGTCTAACAA GCAAGTTAGT GTTAATCAAA AACAAGAACA    120

AAAAAAGGAC ATAAATCAAG AAAAAAAATCA ACTGAACACC TTTAATAAAA ACTTAAAATC   180

TGGCAAGGCT TATTGCTATG AAATTTTTAG AGACGCACTG TTTAATATAA AAAATTGGGT    240

AAATGAAGGT GAAGAAAAAA ATAATATAAA TGCTCTTATT CGGGCATTAT GTACTGATAA    300

TGATGATGCT TTAGAAGATC TTTTTGAAAA GAATGCTGAG CTTAAGAGTA TAGAATATTG    360
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GGTAAATTTT TTAAAAAAAT ATTTCAATAA AACTAATAGA TTTGATGATC TAAATAAGCT    420

TAAAGTATTT ATGTCTGATA ATCGGGATGT TTATAAAACA AAAGTATTAA AATTCTTTTG    480

TATGTTGAAA AAAGAAAGAC AATTTAATTA TATATTTGCA GCATAGCAAT ATTAAAGCCC    540

CCTATTTGGG GGCTGCTATA GGTATAATAA TTAAGGTTTT TATTTTTGAT TGAGAAATGT    600

TTTTAGTTTT GCCAATTAGC TGTAAGACCA GCATAATGAT TATCTTCTTT TAAAAgTTCA    660

yCTTTAAgGT ACtGATAAAT TTCTTCATTA GAATTCTAT TAGaCATATC ATTAGCGACG    720

CCTCTAAAAT aTTGCyCTAy TAAGTTGTCC ACCTCCCCAT ATTTCATTAT TTTTATTACA    780

ATCTTGTGGA GTGTTTTTTT TACAATCAAT AGCTCCTTTA ATATAAGTAT CAAAAGTTTC    840

ATTTTGTGCT TTTGATTTTA AGAAGTTGTA AACCTTGGTA AAAGCACCAG CTAATTCTTT    900

TTGTTTTTGA ATATCTTCAG AAAGCCAATC AAAGAAGTCA TTACATTTAC TTTTGTTTCC    960

ATTCATGCAC CCTTGTATTT CATTGTTTAA TTTTTCAATT GTGTATTTAA ACACATTGAT   1020

TAATGAAGTA AACATTTTTT CTTCGTCGGA TGTTAAAGTG ATTTTTTCTT GTTGTGGCAG   1080

TTCTTCTTGG CTTAAATCAC GTTTTTTCCT GCTTTTTGTT TGTTGGGCAT TGTTTTTTAA   1140

AGTGTCATTA TCATTGGAAT TACAGCTATT TAGTAGTAGC AAAGATATAC AAAATAATAT   1200

GTTGATGATT TTCATTGTTA CTCCTTTTTT TATTATTAAT ATTCACTTAA TCAATTATTA   1260

ATACTAAATA TGGGATAAAC AATTATTATT TGAATTGATA TGTTTTAAGT GAGGTAGTAG   1320

CTATTTAGAA ATGAAAGCAA ATATTAGCCC GGCTATCATT GTGATAGACA TTGCTCCCAT   1380

GATTCCTAAT ACCCATTTAA GCATTCTGT AAGAGACATT AAATTCTTTT CTACATTATC   1440

TATTTTAGCA TCTAAATTAG ATATGTCTTT TTGTAAATTC TTTTCTACAT TGTCTATTTT   1500

AGTATTAAGT TCGCTTTTAA CAGTATCAAT CTTAACATTT AAATTCTTCT CTACAkTATC   1560

AATCTTAGTA TCTAAATTAG ATATATCyTT TTGTAAATTC TTTTCTACAk TATCwATCTT   1620

AGTATCTAAA yTAgaTmTAT cTTTTwGtaA ATTCTTTTCy ACATTrTCTA TCTTGGTATT   1680

AAGTTCACTT TTAACAGCAT CAATCTTAAC ATTTAAATTC TTTTCTACAG TATCTATTTT   1740

AGAAACAAGA TTATCAAATT TTATATCAAA TTGTTTTTCT AAATTTTCTA AATCTCTATA   1800

TGTTAGTTCA TTGTGATAAT ATCTTTTAGA TAAATCTTGT GCTATTAATT GTTCCATGCC   1860

CAGTCTAATA AATTCTTTAT ATATTTGTTC TTGAGTTACA CTTGCAATAT TTGTTGACAC   1920

TGTTTCCATA AAATTTTCCC TTATGGTCAT ATTATATACT ATTTTAGATT AATTGGCTTT   1980

AGAGATTTTT ATATGTAAAG TAGAATTTCT TGCAAGAAAA ACCTTTTTGT AATTTACATT   2040

TTTAACTTCA GATATCAGTT TTAAATTTTT TACTGTAGAT TTTTTACAAA AACAGTATTG   2100
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CAAAAACTCT TAGATTACTT TTTCTTTTCT TTGTATACTA CAATAACTCC AAAACCCACT   2160

AAATGGTTTA GTGATTTAAC CTCAAGAATA TTTTCGGCAC CTATTTGGTT AATAAAATTT   2220

TCTAACCCTA TCCCTATAAT TTCGAATAGA GTTTTGTTTT TATCTTCTTT TTTTATAGGA   2280

AAGTTAATGk TATGCTTATG ATCATCACCG CCTTGATCTA AAGCaTTAAA GTTTTAACTT   2340

TaTAATTTCA TCyTTTTaAT TcATATGAAA TTAAATTACC AATACTGATA ATAAACATAA   2400

aTAACATTAA TAAATTAATT TTTTGcACAT tGTGTTCCTT AATAAATAGA ATATTAACAA   2460

TATTATATCT TTATTAAGAT TTGCCCTAAA ATATAAAATT TTATTAAAAT ATAGCAGTAA   2520

TAAACGACTT TAAGAATATA AATGGGAATT TCTTGCAAGA AAAACCTTTT TGTAATTTAC   2580

ATTTTTAATT GAGAATATTT ATTATAGACT TTTTCCGCTA TTGGTTTTGT TTTTTTAATG   2640

TACTCTAAAT ATATGTTGAG GGTACTCTGA GCTCAGATTT TT   2682

(2) INFORMATION FOR SEQ ID NO: 48:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2532 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CGGCATnACC AGTAAAGTTC AACACTAGAA TATTGCCTTA AATGCACGTA TAAATCCTAA   60

TTTTAAATTA GCACACTCTA TATCTAATTC ACTTATAACT TTCCtAGCGT TAACTTCTGA   120

TTTAAAAGTT TGTGATAAAA GGTGTTCTAA AGTATCTTCA CTAATTGTTA CTCTAGAGTC   180

TTGGTTAACA ACACTTTCTC CACTTTCCCA TTTTTTCCTC ATCCTCCACA CATTTACCCT   240

AGAAACCCCC AATTTATCCG CTATTTCCCT ATCATCTAAC AATCCTTCTC TAAAATATGC   300

AACATAATCA TCAAAGACC TTTTGGCTCT TTTCAAGAAA ATTCTCCTAA AATAACAAAA   360

TTAACAAATT GTTACTCTAA ATAGTAAAGC AATTTGTTAA TTCAATTAAC ATAAATTATT   420

AATTTCTTTA TACCTATTAA CAACTGCCCT ATATTTACAA TATTTATTAA TATAAAAACC   480

AAACATTTCA AATATCCAAA AAGGAGCATT TATATGAATC AAAAACAAAT ATTTTTATTA   540

TTTTTATTAT TTTTAAAAGT AACAATAAGT TTTTCTTATG ATCAATCTCA ATACAAGGGA   600

TATATGGAAA AATATTATCA TAAGAAAGGC AAAACAGATA CGCACATATC CTTTTTTCAA   660

ACTCTTAGTG CTGATGAAGG GGGTTTTTCT ACTATCTTTA TAGGAGAAGA TGAACAATTA   720

AGTCGTCTTA GTTTTACCAC TTTAAAGGAT ATTAAAGACG GCAAAGAAAC CTCTTATATG   780

GGTTTTAACT TAGAATACCA TTACAAAGCA AAGTTTAACA ATCCATACCC TATGTTAAAT   840

1024

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GATATACGTG CAAACATTAG TAAAGTGAAA GTTAAATTTT TTTTTGATAA TGGCCCCGAA      900

AAAATAATAA GAGAATTAAA TCAAAAATTT GTAAATAATA GAGTTATGTG GGAAATTTGG      960

AATAATTCAT ATAATAAGCT TTCAGAATAT ATTAGGATTA ATCTAAGAAC CTCTGATCCG     1020

GGCATAGAAA ATTTACTGCC AAAATTATTA AAACATAAAA CCGTAACAAT AACAATTGAA     1080

ATTCCTGAAA GTGAAGATCC TGAGAAATTA ACTAGTTCTA TAACTTTTGA TCTTGATAGC     1140

TTTCAAAAAC TATACAAGAA ATATAGTACG TATTTTAAAT AATATAACAA GACTCGCTGT     1200

GAGTCTTGTT ATATTATAAT TTATGATTGT AAAAAAAATT TTTCTATTCT TTTTTATTAG     1260

AATCTTTAGA TTCTTTCTCT AACTTTTTAA GCTCTTCAAG CTCTTCTTCA ATCTTTTTAA     1320

GCGAGCTTAC TATTATTTCT TTAGCTATAT CGCTAGTACT ATTACCACTA GAAATATTTT     1380

TAAAGCCCAA ACCCCGAGCA TGCCGCAAGG nTTCTATTCC AACTTTCCCT TGATTTTTAG     1440

CCCTTTCTCC ATCAGTTATT CCAATTGCAG ATTCAACTTG ACCCTTAAGT TCTTCAAATT     1500

TTTTTTGAGA CTCTTCTAAT TCTTTTTTTC TTTTCTCTAT TTTTTCATTT AAAGCTTTCT     1560

CAAGGATTTC TAATTCTTTT TCAAACTTTT CTTTATCTTT TAGTTTTTCC TTTAATTCTT     1620

CTATTTCCTT TTCATAATCA GAATATGTTT TAAGAGAAAC ACTTTTAGGA TCCGACTTCT     1680

CTATCTTATC CTTTAATTCT TTTATTTTTT GTTCAATTTC TTCTTTTAAT TTTTGATCTT     1740

CAGCAACACC TTGAACCACT TGATCTTCGC CCTGCTCCTG AGGCTCATCA GCTTGCATAG     1800

ATTCTTCATC CTTTGGTTGA ACTTTTGCTT CTGGTTTTTT AAAATCTCCA AAAAACTCTT     1860

CTTTTTTTGT ATCTAAAAAT CCCTTAACTT TTCCTTTTAA ATCTTGTTCT AAACTTTTTT     1920

TTACATCTTC ACCACTTGCG TAATTCTTGC AAGAAACTAT CAGCGCAAAA ATAGCACAAA     1980

TAATAAACAT TTTCTTATTC ATAAGTTGCT CCATAAGTCT TAAATCTAAC GCAACACCGA     2040

ATAATTACAA TTTTTCAAAG ATTTAAATAT ATAATTTTGT TACATTCAGC TATTACATAT     2100

TAACAAAACG CAAATATAAT TTTAACCAAC TCCCCAAAAT CTCTCCATTG CAAATGCACC     2160

ACTCATTACA AAAGACTACA AAATCCATAC AACTTAAATT TCAAAGTCTT TGCTATATAT     2220

TAGATAAAGT ATACTGTCTT TCTTATCCGA CACCCTCAAA AAATGCCTAT TCTGTTTATC     2280

ACAGCCACTC CACAACCCAA ATTTCGCATG CAATGAGAAC ACCCAAAATT TGACTAAAAT     2340

TTTAGGTTTT TGATAAAATA TAAATTACAT TTTTATTAAA TTTTTATTAC TTTTACTTAA     2400

TTTAAAAGTA ACACTTCTAA GGAGAGGATT TTATAGATAT GAATAATTAT TTTAATTTAA     2460

ATAATTTCAA TATGGATTTT ATGCTCAAAC TATTTCAAGA TTATCAAAAT GTGGTAAATG     2520

AAAATAAAAT TC                                                        2532
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(2) INFORMATION FOR SEQ ID NO: 49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2528 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

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nAGGATCCCC AGCTCCCttA ATAGCCCCCa TCAGCCTTCC CTTTCTCACC ACCATCCTTC      60

ACAGCAAACT TTCCATCCTT AGCCATCCCC CTCAAAGCAA TAGCAGCAGC AATCTGATCA     120

TCCTTCTTCA TCTCATCCTT AAACTCCGCA CCATTCTCCT CATTACCCTT CCCAATAGCA     180

GCAGCAATCG GATTTGTAGC ATCCCCAGGC TTCTTTCCCT CCTGATCAGC CGCATCAGCA     240

GCCTTAACAA TCGCACTTAA TATCTGCTCC CCACTAACAG CACTAACAGC ACCAGCCGCC     300

TTGCTAGCAG CCTCACTGTC CCCAGCATTA GCACCAGCAC CAGCCTTCCC AAACAACTTC     360

CCTGCCCCTT TATTACTCTC CCCTGTAGCA GCAGCAACTT TCAGCTTTTC ACTCCCCCCA     420

GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCG TCACACTCGC CTTATCAGCA     480

ACCTTTGCAG CACCAGCATT AGCCACAACT TCTCCAATTG CATCAGTACC ACTTGAAGCC     540

CCCTCAGCTG TCTTTACAGC TTTTACCAGC TTATCCAACA ACTCAGCAGC TCCCTTAATA     600

GCCCCCTCAG CCTTCCCTTT CTCACCACCA cTCtTCACAG CAAACTTTCC ATCCTTAGCC     660

ATCCCCCTCA AAGCAATAGC AGCAGCAATC TGATCATCCT TCTTCATCcn TCATsmTTAA     720

ACTCCGCACC ATTCTCCkCA TyACCCTTCC CAATAGCAGC AGCAATCGGA TTTkTAGCAT     780

CCCCAGGCTT CTTTCCCTCC TGATCAGCCG CAtCAGCAGC CTTAACAATC GCACTTAATA     840

TCTGCTCCCC ACTAACAGCA CTAACAGCAC CAGCCGCCTT GCTAGCAGCC TCACTGTCCC     900

CAGCATTAGC ACCAGCACCA GCCTTCCCAA ACAACTTCCC TGCCCCTTTA TTACTCTCCC     960

CTGTAGCAGC AGCAACTTTC AGCTTTTCAC TCCCCCCAGC AGCTTCAACA ATCTCCTTTA    1020

TCCCCTTAGC AATCCCCGTC ACACTCGCCT TATCAGCAAC CTTTGCAGCA CCAGCATTAG    1080

CCACAACTTC TCCAATTGCA TCAGTACCAC TTGAAGCCCC CTCAGCTGTC TTTACAGCTT    1140

TTACCAGCTT ATCCAACAAC TCAGCAGCTC CCTTAATAGC CCCCTCAGCC TTCCCTTTCT    1200

CACCACCACC ACTCTTCACA GCAAACTTTC CATCCTTAGC CATCCCCCTC AAAGCAATAG    1260

CAGCAGCAAT CTGATCATCC TTCTTCATCC CATCATGATT AAACTCCGCA CCATTCTCCG    1320

CATCACCCTT CCCAATAGCA GCAGCAATCG GATTTTTAGC ATCCCCAGGC TTCTTTCCCT    1380

CCTGATCACC AGCAGCCGCA CCAGCAGCCT TAACAATCGC ACTTAATATC TGCTCCCCAC    1440
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TAACAGCACT AACAGCACCA GCCGCCTTGC TAGCAGCCTC ACTGTCCCCA GCATGAGCAG   1500

CATCAACTTT CCCAAACAAC TTCCCTGCCT TTTCATTGCC CTCTTTAGCA GCAGCAACTT   1560

TCAGCTTTTT ACTCCCCCCA GCAGCTTCAA CAATCTCCTT TATCCCCTTA GCAATCCCCT   1620

TCACACTCGC CTTATCAGCA ACCTTCGCAG CATTATCATC AGCCACAACT TCTCCAATTG   1680

CAGCAGTACC ACTTGAAGCC CCCTCAGCTG TCTTTACAGC TTTTACCAGC TTATCCAACA   1740

ACTCGCCAGC TCCCTTAATA GCCCCCTCAG CCTTCCCTTT CTCATCATTC TTCACAGCAA   1800

ACTTTCCATC CTTAGCCATC CCCCTCAAAG CAATAGCAGC AGCAATCTGA TCATCCTTCT   1860

TCATCTCATC CTTAAACTCC GCACCATCCT CATTACCCTT CCCAATAGCA GCAGCAATCG   1920

GATTTTTAGC CTCCCCAGGC TTCTCTCCAT CCTGCGCAGC CTCACCAGCA GCCTTAACAA   1980

TCGCACTTAA TATCTGCTCC CCACTAACAG CACTAACAGC ACCAGCCGCC TTGCTAGCAG   2040

CCTCACTGTC CCCAGCATTA CCAGCACCAG CCTTCCCAAA CAACTTCCCT GCCTTTTCAT   2100

TATTCTCCCC TTCAGCAGCA GCAACTTTCA GCTTTTCACT CCCCCCAGCA GCTTCAACAA   ·   2160

TCTCCTTTAT TCCCTTAGCA ATCCCCGTCA CACTCGCCTT ATCAGCAACT TGGCTTTTAC   2220

AATTAATAAA AACAAAGAAA GTTGTTAATA AAATTGCACT TGAAATTTTT TTCATATTTT   2280

TTTGTTTAAT GATTGTTTTG AACATTTAAA AAATGTTTTT GTTAAGAGGC TTTTATTCTT   2340

TGTTTAAGTT AAAGTTAAAT AATAATAACT AGTTTTTTTA ATTGGATTTG TGAATTTTGC   2400

CTACTTCCGT ATCACATATA ATAAAGTTTG ATGACATATA TAGTATTTTT ATTGCTTGAG   2460

AGTTTTAACA AGTGTAGGTG AGAGAATTTT TCATTTCTTT TATTATAAAG AATAAAAGAA   2520

ATGAAAAA   2528

    (2) INFORMATION FOR SEQ ID NO: 50:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2496 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

    TGCAGGTCGA CTCTAGAGGA TCCCTGCCTC TTyaAGTATG CTAGCCAAAA TATRaCGAGT   60

    AAwTTCTTTG TCTGATACTT TAAATTCTTT GTCATATATA TTTTTTkcAA TTTTAAATAC   120

    TATAGArTCA TCAGGcTcTC ATAAAGyATC TCTCTAAGAG TTTTTTGAAT TATmTCTTTT   180

    TCtTTrgAtA TTTGyTCTTT TTCAACTGmT ATTAyATTrC TTGTyTTTAG GTATCTTTCT   240

1027

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TTTCTTATAA GATAGCTAAA TAAAATAAAC CATTCTTGCT CTTTATATTC TTCTTTtTCT      300

TTAATTTTAG AAAAATCAAA TTCAATATAT CTTTTTTCTC CATAAAGTAC TTTCGATTTA      360

TCATATAATC TCCATACCTT TCCATTTGAA AGTATCCCAT AATGTTTTTG ATATTGATTT      420

AGATATCTGT ATAGCTGATC TTCTGCTTCT TTTACCTTAT CTTTAGCATC AAAACTAAAT      480

GATGGACGCT TAACTTCTGC TATAAGCAAG ATATCTTCAG TTGGAATAGA TTCATTATTT      540

TTTTTAGCTT CTTCTAATTT TTTATTAAAA GCTACTTTAT CTTTATCATT TTCAAAAAGT      600

AGTATATCTA CTCTGGATTT TACTCCTTCT ATTTGCCCAC CTTTTTGTTG TTCTACTGAA      660

TAAGCTAATT CTTCAAATAT AGACTTTAGC AAAGACTCTA TATTTGCTTC TGTTGAATTG      720

TCATCTATAG CTTGAATTTT ATTTTTTAAA AAAATAAAAA AGTTTTTTGA TTTAACAATA      780

TTTTCTTTTT TTATAAAGCC TTTTGACAGT TCTTTATAAA GAGATACATT TGGATCATTT      840

GTTTTTATAA TGAATCGGCT TTCATTGTTC ATATTTACAA CCATTATGTT ATTTATAAAT      900

CCTTTTTAGC CCTTCTTGAT ACTCGAAATG TACTCTAAGA TTAGTTTTTT TAAAATTAAA      960

AAAACTAATC TTAGAGTAAG TCGGCCAAAA CTTGTTTTAA TATTTATTTG ACTATCAATA     1020

CTCTATCTTT AGAATAAGCT TGTTAAAAAT TATTTCTCAC TTTTTCTCAA TTAATTAAAG     1080

TTATTAATTT ATTTTTTATA AGGCATCCTT AATTAAAGAG CATTTAAAAA ACACTTTTTT     1140

AAAACCGAAT TTTTCTTAAA CATTCCCCAA TTTGTGAAGC ATAAACAAAA AAATGTTTTT     1200

ATCCTTTTCA TTTTCAAAAT TACAATTATA GAGTCTTTTG TTAATTTCTT CTTTAAAAAC     1260

ATCTTGCTCA GAATCATGCA AGCAACAAAG ATGCAAAAAA TTTTTAAAAG AACTTATCAG     1320

GTCAAAAACA ACACAAATAA TAACCCAGTT TTTATTCATA ATTATCCTCT CTCAAAATTA     1380

AAAAATAAAT CAAAGTCTTT GATTACAAT TTTTTATTAA GCAGTGAAGG GGGAAAAACA     1440

AATTGTCCTA AATATTTAAC AAAAAATGGA AATAGACTTA ATAAACTTGG TTTTTTCTCA     1500

GGAAGGATTT CTAATTACAA CATCAAATTC TTCCTGAATA TCTGGAAACT CAATTCCATA     1560

GTAAAAAAAT TTATAGTAGC CGCTTAATTT TCTAATTATA TCTATTTTTT CTTTATCTTT     1620

ACTAGAAGTT TTATTGCCTA AAATATTTTC AATTAAACTA ATTAAAGCTG TAATATCACT     1680

AAATTTTATA TTTAAAGATT TGTCAAAGA TAATGAATAA AGTTTAATTA AAGAAAATAT     1740

TATTCCTAAA TTATCTGTAT CTTCACTTTT CTCATATTCT TTATATATAT TTTTAGATCT     1800

TTCTATATCT TCTTTAGCAG TATCGTTAAT ACCTCTAATT TTTTGATAGC TATATTCTAA     1860

AATAATTGTA ATTTCTTTAA TTCTCTTTTT AAATAAAGAA AATCCACCTT CAAATTTCTT     1920

TTTTTTAATA TCAAAAAATT AATCTTTGGC ATATCCTAGT AAAGGATTTC CTACTTTTAT     1980

ATGATGTTCA ACAAAGCTTA ATGGTGTTCC AAAAATAAAA TATTTTAATA ATCTAACTTA     2040
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TTTTTTTGAG ATAGTTTTTT ATAAAACTTG CCCAAGCAAT CTATACTCTT AAGTTCGGGT   2100

TTTCTCAATC ACCTATAACT TTATTTGCTA ATTAATTTTT TATAAAAGCT ATCCTTAAAT   2160

TTTTCAAAAT ATACTATATG AACTACTGCT TAAAAAGCAA AGACTATAAA ATAAGTAGTT   2220

CATCAGAAAG TTTTTGATGG TATTACTACT ATTAATAGAA TTTAAAAAAT CGAGCTTACC   2280

AATGTATTTA AATAAACTAG AAAGCAAACC ACAATACATG ATTAAAATGA TATGGGCAAT   2340

AAACTTAAAA AGTTTAACGA TAATTTTGAA ATTCTTATTA GAATCTAATT AAAAATGTAA   2400

ATTTATATAA ATTTTATAAA TAAAGAGTCA AAGAAACGC TTTATACTAG AAAGTCTTTA   2460

TAAAGATAAT AAAATATATT TTTTAGAACT TTCTTC   2496

(2) INFORMATION FOR SEQ ID NO: 51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2487 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ATTTATTTAC ACGAAACCCT GACTTTTTGA GAAGATTTTT GAATTTATTA GAAATATGGA   60

TAATGCTAAT TTGGTTGTCT TTAAACTTAT GTTTGGATTT TTGAAAAAAA TAAGTACGTC   120

TTGTATCAAG ATTTTTCTCA TTAAAATGAT TTTTGTGTGC TGTTTGGATA GCCTCGAACT   180

CTTCTGAGTT GATAACAATT TCTCTAATAC AAGTTACATT TCTTTTTTTT GCCACATTTA   240

CTTTTATGTT GTATAAAGTT TTTCCATTTT TGCTTAAAAA AGTTGAAATA TCTTGCATTT   300

TTACTTTTTG CAGTTCGGTG CCCCTGCAGC CACTTATTGC GAGTAAATGT AAAAACCAAC   360

CAGATATTGG ATCAGCTTGT TTAAGAGTTT TGATGCATTT TTCAATTAGT TTGCCAATTT   420

TTGGGGTCAA ATAAAATTTA GGAGTTGGCT TTGAAGCTTT TTTAGTAGGC TTAGAAGAAA   480

TTTTTAGTGA ATTTTTAAGA ATTTTGTTTT CATTTATTAG TTTTTGATGA TCTTGTAATA   540

ATTTAAGCAT AAAATCTATG TTGAAATTAT TTAAATTAAG ATAATTATTC ATGTCCATAA   600

AATCCCCTCC TTATAAGTGT TACTTTTAAA TTAAGTAAAA GTAATAAAAA TTGATTAAAA   660

ATGTAATTTA TATTTTACCA AAAACAAAAA AATTTAGTCA AATTGTGTGG CTTCTCATTG   720

CATGCAAAAT TTGGATTGTA GGATAGCTGT GATAAACAGA AGAGGCAATT TTTAAGGGGT   780

GCACTTAAGA AAGATACTAT ACTTTAAGTG ATATATAGCA AAGACTTTGA AATTTAAGTT   840

GTATGTGTTT TGTAGTCTTT TATAATGAGC AGGCCATTTG CAATGGAGAG ATTTTAGGGA   900

1029

GTTGATTAAA	ATTATATTTG	CGTTTTGTTA	ATATGTAATA	GCTGAATGTA	ACAAAATTAT	960
ATATTTAAAT	CTTTGAAAAA	TTGTAATTGT	TTGGGGTTGT	GGTAAACTTA	AGGCTTATGG	1020
AGTGGATTAT	GAATAAAAAA	ATGAAAATAT	TTATTATTTG	TGCTGTATTT	GTGCTGATAA	1080
GTTCTTGCAA	GATTGATGCA	ACTGGTAAAG	ATGCAACTGG	TAAAGATGCA	ACTGGTAAAG	1140
ATGCAACTGG	TAAAGATGCA	ACTGGTAAAA	ATGCAGAACA	AAATATAAAA	GGGAAAGTTC	1200
AAGGATTTTT	AGAAAGATT	TTAGATCCAG	TAAAGGATAA	AATTGCTTCA	AATGGTCCAA	1260
TAGCAGATGA	ATTGGCAAAA	AAATTACAAG	AAGAAGAAA	GGTAAATAAC	GGGGAAGAAG	1320
AAAATGATAA	AGCTGTCTTT	TTAGGAGAAG	AATCAAAAGA	GGATGAAGAA	GAAAATGAGC	1380
AAGCTGTTAA	TTTAGAAGAA	AAAAATGCGG	AAGAGGATAA	GAAAGTTGTT	AATTTAGAAG	1440
AGAAAGAATT	AGAAGTTAAA	AAAGAGACTG	AAGAAGATGA	AGATAAGAA	GAAATAGAGA	1500
AACAAAAACA	AGAAGTGGAA	AAAGCACAAG	AAAGAAAACA	ACGACAAGAA	GAAAAGAAAC	1560
GAAAAAAACA	AGAACAGCAA	GAAGAAAGA	AACGAAACG	ACAAGAACAA	AGAAAAGAAA	1620
GGAGAGCTAA	AAACAAAATT	AAAAAACTTG	CGGATAAAAT	AGATGAGATA	AGTTGGAATA	1680
TTGATGGTAT	AGAAAGTCAA	ACAAGTGTAA	AACCGAAAGC	AGTTATAGAT	AAAATTACGG	1740
GGCCTGTATA	TGATTATTTT	ACCGATGACA	ACAAAAAGC	TATATATAAA	ACATGGGGAG	1800
ATTTAGAAGA	TGAAGAAGGC	GAAGGATTGG	GAAAATTATT	GAAAGAATTG	AGTGATACTA	1860
GAGATGAGTT	AAGAACCAAA	TTAAATAAAG	ATAATAAAAA	ATATTATGCC	CATGAAAATG	1920
AGCCTCCTCT	AAAAGAAAAT	GTAGATGTCA	GCGAAATTAA	AGAAGATTTA	GAAAAAGTAA	1980
AATCAGGATT	AGAAAAGGTT	AAAGAATATC	TTAAAGACAA	TTCTAAATTT	GAAGAAATTA	2040
AAGGATACAT	CAGTTACAGT	CAGTAATTAT	ATTGGATGCT	TTTAGATGTA	ACTAAATTTT	2100
ACGTACACAA	AATAACAGCT	AGTAGAAAAG	TTCACTGGCT	GTTATTTTTT	TGTAGATTTC	2160
ATTGTTATGA	ATATAGAAAT	GTTTTCTATC	AAAACTTTCA	TTTAAAAAGT	GCAAAAACTA	2220
TTGCTAAAAA	TGTTGTTTAT	TTATATACTC	TCTAGAGCTA	TGACGTATAC	AAATGAGATT	2280
TCAGATTTTG	ATGATAATTT	ATATAAGAAA	ACAAAAAAAG	AAATAGATAA	ACTTATAAAC	2340
AAGCTCTATT	TAACTAGCCn	AATAACTCTA	AAGCAAAAAA	GACAAATnTA	CAGTGCTGTT	2400
GAAAGAATGC	AAAAATACGT	AATAAAAACC	GGAAAAGTG	TTCTTTTAGA	ATCGGAAAAA	2460
GAATTTGTTA	AAGACACTTT	GAAAAGA				2487

(2) INFORMATION FOR SEQ ID NO: 52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2462 base pairs
        (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

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AGGAGATAAG TTTATTGGTA TTTTTTATGG CTATAGAAAC CCAATCAAAA cCTTTAATAA       60

AGTATaAAAT AAATGGAACT AGAAAaGCAT ATGCATTAGC AAGAGCaTAT TATATGGAAT      120

TTAGATTTAA AGCCgGAAGT GTTTTTTGCT ATTTTAAGGG CTATATCGT TTATTGGATA       180

AAAAAAGAAC AAtAATCaTT ACAACAAAGT TTTATTTAGT ATGTTTGCaG ATTTAGaACA      240

ACAAGTATAT AAATTTTATG GGAAAAmATA CCCGGAGCaA GGACCGTTAA TAAAATGGAT      300

AATAAAAAAC CTAAAATAAT AACAATAGCG TCAATCAAGG GCGGTGTTGG TAAAAGCACA      360

AGTGCCTTAT TTTATGGCAA TATTTTAGCT AAAGAAAGAC ATAAAGTATT GATAATTGAT      420

AGTGATCCAC AGGCCAGTAT TACTAGTTAC TTTTTGTTTA AATTAAAAGA ACAAAATGTG      480

AATGTCGAAA ATTACAATCT TTATGAAGTT TTTAAACAAA GAAAATATAT AGAAAATTGC      540

ATTTTTACAG TATCTAATTG TTTAGATATA ATTCCCAGTT CCTTAGAATT ATCTGTTTTT      600

AATTCAGAAA GCATACCATT ACAAGACAAC CTTTTAGAAA AAGACTTTT GACTATTAAA       660

TCTAAATATG ATTATGTGAT AATCGATACA AATCCCAGCT TAGGACATCT TTtAAACAAT      720

GCTTTAGTAA TTACCAATTA TTTAATAATA CCAATTAATT CCGATTTATG GGCAGTTGAA      780

AGTATAGATC TAATATTAGA TGCAATAAAT AAAGTTTATA GAAATGATAT TACACCTTAT      840

TTTTTAGTGA CGGGGGCACT AGAGAGACAA AACATAGATA AGGAAATAAT ATTTAATTTG      900

GAGAATAGAT ATAAAGAAAA TCTAATAGGA GTTATTCCTA AAAGAGATGA TATCAAAAAA      960

GTGCTGTTTT ATAGAAAAGA ATTTTCTTCA AAAACAGACT ATTATCAAGA ATATAAAAAA     1020

TCTTTAGATA AAATGTTAAA AATAAAATAA CAAATAAAAT ATATCCAGTA ATGGACAAAT     1080

AAGGAGTTTG CATGAGCATT AAAAATAAAA TGATAATAAC CAAAAGAATA GATATAAAGG     1140

AAAATATGTC TAAAATGGAG TCATTAGAAG AAATTCATAA AGAAGAATAT TTGAGATTAA     1200

AAGACAAATT AAAAACTCTA ACAACGGATG ATATTTATAA TAAAATAGAA ACAGCAAAAA     1260

TATTAAATGC GATTAATCAA AAAAAACTGT ATATTTTAGA CGGATATAAA AATTTTTATA     1320

GCTTTTTAGC TGATTTTAAA ATCGCTAAAT CTCAAGCATA TAAATATATA AAAATAGTAT     1380

CGGGCGTAGA AAAAGGTATT ATTGACTATA ATTTTATTGC TAATAATGGC ATTGAAAAAA     1440

CAATTAAACA ATTGGAAAGT AACAATGTTA TTAAAAAATC TAGGCAAAAT CCAATAAAGC     1500

CTTTAAGGTT TCAACTTAAA AAGCAAGAAA GTTATGATTT TTATAAAAAA AATGGGAAGT     1560
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1031

TTACTGGGTT TTTATTGGAA GAACTTCTTG AAAGTCAAAC AGATTTGATT AATAAGCTTT 1620

TAAAAAAATA TAAACAATTA AAAGGATATT AAGAGGATTT TATGAGAAAT TTGGTGCACA 1680

GAACATATGA TATAGAAAGC ATAAAAAATG AATTTTTAAA CATAGGATTT AGTGAAGAGG 1740

CAATAGATTT TGTTTTTCTT CATAATGATA ATTACAACTA TGAGGTTTTA AAAGAGAAAA 1800

TAATTGATGT AGAAAGAAT TTGCAAAAG ACATATCTAG TTTAGATACT AAGATAGATA 1860

ATGTAGAAAA GAATTTAAAT GTTAAGATAG ATAATGTAGA GAAGAATTTA AATATTAAAA 1920

TAGATAGTGT TAAAAATGAA CTTAATTCTA AAATAGATAG TTTAGATACT AAGATAGATA 1980

ATGTAGAAAA AACTTTGCAA AAAGATATAT CTAGCTTGAA TACTAAAATA GATAGTGTAG 2040

AAAAAACCTT ACAAAAGGAT ATATTTAGCC TAGATAATAA AATAAATGTT TTAAAAAACG 2100

AACTTACTGC AAGTAATAGA ACAATACAAG TAATTTTAAT AATGGGAATA ACGCTkGCTC 2160

CAATTATTTA TTCTATATTC AATAAGCaTT TTTTAAATTA AGAaTGATTA rAaTTTTATA 2220

AaGTAATAAG TTAGTATATA GCTTtAAAGT AGAACTTATT TGAATTTTTT AACAAGAGAA 2280

TTTAAATAGG TTCTTTTATT TTAACAAATA CAAAATAATT TTAATTCTAA ATTGAACTGA 2340

ATTTAATTGT TTAGTGAGTT TATCTAAAAT AAATTGAGCT AAGCCAGCGG CTTTCTTAAG 2400

CTCTTTAACA TGAGAATTTA ATAAAGCTTT TATTTATTAT AATAATTTCT GTAAAAAGCn 2460

TG 2462

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

AACCCCnAAA AAGGGCTCCC AATATTAAtw GAGAGATTTA TATTTTTCrA ATGTTGTGCT 60

AGCTTTTATy TCATTATTAT TGAATATAGG AGTAACTAAT GAGAAATAAA AACATATTTA 120

AATTATTTTT TGCAkCAATG TTATTTGTAA TGGCTTGTAA AGCATATGTA GAAGAAAAGA 180

AAGAAATAGA TTCATTAATG GAGGATGTTT TAGCTCTTGT AAATGATTCT TCTGGAGGCA 240

AATTTAAAGA TTATAAAGAC AAAATAAATG AATTAAAAGA AAATTTAAAA GATATAGGCA 300

ATGCrGAGCT TAAAGAAAAA CTATTAAATT TGCAAAATTC CTTTCAGGAT AAATTAGCGG 360

CCAAATTAGC AGCGTTAAAA GCAGCTAAAA ATACCATTGA AAACATTACT GACAAGGATC 420

AGGATATTTC AAAAAGAAAA ATATGGTCAG AAGCAAAATT AGTTGGAGTA ACTGTACCAC 480

TTCTTGGAAG CAATACTTCT GGTAATGGGG ATAAAATGTC TAAAAACGCT GTAGAACAGA   540

TAGACAAAGT AATAAAGTTC CTCGAAGAnG GCACTAATTA ATTAGCAAAT ATTCCTGTTG   600

AAAATGTTAA AATCTAGATA TTAAATCTGC GTCAATCTAA TATCTAGATT TTTCTTTTGT   660

TGCAAAAGCC GATTTGATCA TAAATTAGAA TTTCTTGCAA GAAAAACCTT TTTGTAATTT   720

ACATTTTTAA CTTCGAATAT TGATGATATA CTTTTTCCGC TATTGGTTTT GCTTTTTTAA   780

TGTACTCTAA ATATATCTTG ATGTTATGTT TTACCGCAGt ATAGAGTGTT CGTCTTTTAG   840

TGTTGATAAG TCTGGATAAG GATATTCTGG ATAATTGGGG TCATTAACTT TCACTTTTGT   900

TTTAGCTAAA AATGTTACAA GATACATAAC ATATTCTGAA AGTTGTGTTT CATATTTAGC   960

TAAAGATTTT AGCGTTGGAA TAATTGGCGG TTTTGGTTCT TCTGGTAGGT TAGCAATAGT   1020

GGTGCAACAT AACAACAAAA CAATTAGTAA ACAATGCAAT CTTTTAAGCA TTTTCACTCC   1080

TTTTAAGCAT TTTGATGTAT TCTTTCATAA TTTTGTTGCG TTTTGCTTTA AGTGAAGTGA   1140

TAATTTTTTT ATTTTTGTCA TAAGAGATAG CCTCTATTAT CTCAATATTG TATTTTAAAA   1200

TGTCTTTTAT TTCTTCAAAT ATTTTAGTTG AyTCAGCTGT TTCCATAGAT TTTAGTGTGC   1260

TTATATATGT TTTATAGAAA AAATCTATTA CTTTACTAAA AGTATTAATG TAATTATGAT   1320

CTATGTTTGT ATCAGTTTTA GCTATGTTAG TTAAGCTAGA TAGTAAATTA AGTCCCAATT   1380

CAATAGTGTT CTTTTGCATT ATTTGCTCTC TCTTTGTAGA TAGGTTTTCC GTCTTTATTG   1440

AATTTTAGAT CATTGGATAT TTTTAGATTT TTATCATTAG AATTAACCAA ATCAATAACC   1500

GTATTGATTT TTGCATTTAA AGGAGCGAGT GCCGCATTTA TTGCTGGGGT TAATGCACTC   1560

TCAAGTCTTT CCATATTTGC TGTATAGATT AATTTATAAT GAGAATACAG CTCATAAACC   1620

AAAAAGAATC CTTTATGTGC AATTTCATCA AATTCATCTT CAAATTTAGA AAATATATCA   1680

ATAAGGGTTG ATAAAGACGT AAGTCCAAGC TCAACATTAT CTTTGGATAA TTTCATAAGT   1740

TAATCTCTTT TTTTAATGTG ATTTTTGCCA TTACCATTAC CATTCTTAAA AATCTTGCCT   1800

ATTACAATAG TCAATATGTC TTTTAGTAAA GGCTTGAGAA GAATTAATAC TCCTAAAACC   1860

AACACTGTTA CAAAAATCAT TACGGCTATA AGTTAATTT CGTTTAAATT GATAAGAAGT   1920

TCTGTTAATT TAATAGTATC CATTTTTTAA TCCTTTATTT TAATTTTTTA TTTGTATATA   1980

CATTATATAT CAAAATCGTA ATTTTTGCTA AAAAAGCTTA CAGTTTTAAA AGATCTGGGA   2040

CTGAATCTCC ATACATGTAG GCTCTTTTTT GGATATACCA TCCGTTATAA ATGGGAGTTC   2100

TGGTGAATAG TCCGCGAGGG CCCGTAATTT CATAAACCCA ATTGTATGTA ATTTCATCAG   2160

AATACATAAG TTTTAATGAT TTTTTCTGCA TCCTATTATC ATTGATTTTT ACTTGAATCT   2220

CAATATCAAG ATAAATGGGA TCATTATCGT AATTTTTGTA AAAAATAAGA GTTACATCAT   2280

CATTGTCTTC CATATTAATA GATATCGCTT TATTCTCATA GTCAGAAGGA TAAAGTGTAG   2340

TACTTCTAGT TATGCTGCCA TAAGTAAAAT TTGATGGTAC TCCAAGTATA TGTTTAGGAA   2400

CnGGTGTTTT TTGAATAGTA TCTGATGAAG GCATTATCAA AAGATCA   2447

(2) INFORMATION FOR SEQ ID NO: 54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2401 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TATTATTATA TTTAGGGAGA GAATTTATAA AATAAAGCAT AATTACTAGA ATACTTGTTT   60

TTTCTATGAA TGATTGTAAT GCGGATCTTA ATATTAATAA TTATAAAACC AAAACTAAAG   120

ATGGGTTTTA TGCTTTAATT TAATTAATTT TAAGGAAAAA CTAATTACCA TATTAATCCC   180

AAATATATAA TTATTGACAA AAGTTGTATC AAGGGATATT GCCTAATATA GCAGAAGTAT   240

ATTCTGTTAT TAAATATCTC CTAAGGAGGA TTTTATTTTT AAAATAATAG AAAATAGTGC   300

ACTTATTTTA ATAGATATAC AAAATGATTT TTTAGAATCA GGCACTTTGC CAGTATCTAA   360

CAGTAATGAA ATAATTTCTT TGATTAACCA ACTTCAAAAT TATTTCAAAA ACATTATTGC   420

CACCAAGGAT TGGCATTGTA AAAATCATGT AAGCTTTTCT AACAATAAAA ATGGGGGTAT   480

TTGGCCTGAG CACTGCGTCA AAAATACTTG GGGATCAGAA TTTCCTAATG ATCTAAATAC   540

GAAAAGAATA AAAAAAGTTT TTTTTAAAGG AACCGATCAA TATTACGATA GTTACAGTGG   600

ATTTTATGAT GATTGCATTA AAAAAAAACA AACGGGCCTT CAGCTTTATC TGAAAAACAA   660

TTCAATCAAT ACATTATTTA TAACGGGACT AGCATTGGAT TTTTGTGTAA AAGAAACAAT   720

ACTTGATGCA ATTAACTTGG GATTTCGAGT TTATCTAATA ACAGATGCTA CAAGAAGCAT   780

AACATCTACT CCTGAATTAA TAATTCAGGA ACTTAAAAAG CTTAATGTAT TAACTTGCTT   840

CTCCAAGGAC ATCTTCGACA GCCAAAGTAA GCTTAATATA TAAAAAATCA TTCAATAGTA   900

TTTAATTAGA AAACTACTAT TTATAATTAA AACTATCATG GAATGATAGT TTTTTAGACT   960

ATATAAGAAA AGTTTATTCA CCAAAGAATG GCCTTTATAT TAAATTAAAG CCGCCTTTTC   1020

CTTGGTTTTT ACTTCTTAGT AAGAATAATT TTAAGATTCA TAGTTACATT TATATCTCTA   1080

TCATATAAAG CTCTGCAATT AACACAAGTC AACTTAATAT TACTTATCCT TTGTGTAATA   1140

CCACTTCGAA TGCCCTATTT AAATATAATA AAAGAATGAT AAAGAACTCA AATACTTCCC   1200

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CCATGCATCA TATAAAAATA TCCATCTCAA AATGTTAAAA ACAACGCCAC CGACATAATT          1260

CTCTAATACC CAATGTACAG TCTATAGATA CAATAAAATC TTTTAAGAAT TTAATTCCAA          1320

TAACACCTGT TTAAACCGGC TCACAATATA AAAAATTTTT ATTTTTTAGT GATAAACTTT          1380

ACTTATCTGA AAAATTGCTT TATTATGTAA GAGTGTATAA AAAACCATCC GAAGTTGAGG          1440

AGGCAGAAGT GAAGGTTAAT AAATCCCTAC AAATACAAAG TAAATATCAA CACAAACTAA          1500

TTGCTTTAAT TGCGACACTT GAGTATATTA ATAAAAACAA AAAAAAATAC AACCAATCAG          1560

ACATCCTTTA TTGTTTTAAC AGTAACTTAA GGCGCAACGG GCAAAAGAA GTTTCAATCA           1620

AAACGCTTAG AAACTACTTC TATAAACTAG AAAAGCTAAA TATTACTATT AACTACTATA          1680

GACATCTAGG TATTAATATG GGCACTGAAA TCTACTATGC TCTTAGGCAT TCTAAAAAG           1740

ACTGCTATAA TCTACTAAAC CAACACTTTA GGAATAAAAA AACAGAAAGA TTTCAAAGAC          1800

GTGTTAATGT ATATATTAAA ATAAATTACG ATAAAAAGGA CAATGTAAAA AATGGGGAGT          1860

GTCTTAATAA TAAATATAAA AAAGAAGAAA GAGAAACCGA AAGAAAAAAA AGGATTAATA          1920

AGCTTAAACT AAAAAAATAT GCAAAAAAAT GTAATTTCGA TAATGAAATT TCCTCTTTTA          1980

TTATTAATCT TAACTTAAAA AAAGAAACAA CAATCAAGCT TTTTAAATTT ATAATCAAAG          2040

AAAAATATTA TTTCAAAAAA GAAACAAAT GTAATTTACA AAAAACACTG CAAAACAAAA           2100

AAAGAGATTT AATTTCAATA TTAAGAAAAA CCCAAAAAAT TTTAATAAAA GAAGGTTGCG          2160

ACAAAAAAAA GATAAAAACC CAAATACAAA ACACATATCA AAAATATAAA AACAAACCCC          2220

ATTTCATATT AGAAAGCAAT AAATATAAGG ATTTCGATCA AATTATAAAA AAGATAAAGG          2280

ACGATACTAA TAAAACCGAA CCCCAAAAAC ATAAAGACAA TATAGAAACC AATATATATA          2340

ACATACTTTT AGATCAATTA CATAGAAAAA CCAACACAAC AAATTTAAGG TCGGGGATCC          2400

G                                                                          2401
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(2) INFORMATION FOR SEQ ID NO: 55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2324 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```
CAATATGACA TCCTGAGGAC CTTTTATGGA GACTTGTAAA GCTTTTTATT TCTAATGTTT          60

TAGCTTTTAT AAAAACACCA ACCATGACAC ATATTGAATT TTTAAATCTA TAAACATTAT          120
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1035

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TTCCTTAAAT TTCTAAAAGT TTTTTAGGCT CTGTATTTAA AAAAATCACT TCACCAAGAA        180

TAACCTTTTC ATCATTTAAT AATAATGTTT TCTTGCTAAG AAAATTTATA AATCTATTTA        240

AAATGCTTAA TTAAGCTTAT TTGTTTTCAA ATAATTCTCA TATCCTTTTA TTAAAAACAA        300

AATGTATTCT TCTCCCTTTT TATTTTTTAG CACCTCAAAA TCATTAAGCA AAACCTCAAA        360

ATCTTCTTTG GTTAGCGAAT AAAGACTAGC TACAATAAAG TTATTTTCAT TTTCTTTTTC        420

TTTGAAAAAT TCATCTTTAG TGTCTAATTT TAGAATTTTA TTAACTTTTT CTTTGCTAAA        480

TTTAAAATGC TCTAAGTAAA GCAAATTAGA GAAATTTAAA GGATCATTTT TAGCTATTAA        540

CAAGGAAGTG TTTTTTACTA AAGTTAAGTA TATCGGATTA GCTAAAATTT CTTCTTCTTC        600

GGGTTGAGGC ATAGGGCATT GATATAAGCA TGATTTTACA ATATCAGTGC TTAAAGCAAA        660

TCTTCTTATT AAATAGTCAA AAACAAATGA ATTAAAAATA GATATAATAA ATAATTTTTT        720

ATAAATAGAT ATTGGTGTTT TCTCATAATT TATATATATT GTAGAAACAC AATAACAATT        780

TCTAGGAGAT AAAGTACTAA TCATGGTTCT TATATCTGTA TTTCTTGCAA TCCTTCTATA        840

TAATATTTTT TCTATTTGAT ACTGATTGTC TTTAGTTGAT ACTTTTTGAA AGTCATCTTT        900

ATCTATCCAT AGTAATTTAG AGCTTTCTTT TGCATCTTTG TCTTCAAAAA ATCTTGAATT        960

AAACTGATGA ATATTAGCTC CAGAATAAAG AAATATAAAA TTTTCATTAT TATATTCTTT       1020

ACATAGTGTT TTATACTTTG TTAAATTTAG CCCTACTCCA AAATTAATAT ATTCTTCACT       1080

AAGAGTACTA AATTTGCTAA ACATTTGTT AATTAAGATA AGCTCTTTAC TATCTTTAAA       1140

TTCAATAATT GATTCTTGAA TAGGAGACAG TTTTTTAATT TGCTCTATAT CTAATTTAAT       1200

TCCTTTATAA GGATCATCTT TATTATTTTC TAAGTTACTG GTTATTTCTT TTAAAATATT       1260

ATCATTACTC TGAATCATAA ATTTTGCTTT AAAATTCGAT GTAGGAGTTT TAGTATTGCT       1320

TATTTGAAAT ATTGCAAATT TAAAAAGTGT TGCCACATCT TTAAATCTTT TTTGATTTTG       1380

AAATTGATAA ATATAGTTAA GCTTATAGTT AGTAAATATA TATTTTCTTA GTATCCTAGC       1440

ACTAGATTCA CTCCAAAGAG CTGAAGGAAC TAAATAGGTT AAATTTCCGT TTTCTTTTAT       1500

TAATTTCAAA TTAAATGCTA CAAAATATCT AAAAAGATTT GGATCACCAC CACTAGCAAA       1560

ATTTTTAAAA TCGCTTTTAT AAAGATTGTT GATAGTACCC ATACTATTTT TTTCTTCATT       1620

GTATTCAATA TTCAAAGGAT GATTATCTCT GCCAAGTATT TCTTGCTTTA TTTTATTTTG       1680

TTCTTTTATG CTTAGCTTTC TATAACTGGG AATATGTTTT GAGAAAAACT CTGCTTCATT       1740

AAACTTAGTT TTTTCCCATG GAGGATTTCC AATTACAATA TCAAATCCTT CTTGAATATC       1800

TGGAAACTCA ATTCCATAAT GGAAAAATTT ATAGTGGCTA CTTAATTTTC TAATTTTCTC       1860

CATTTTTTCA TTATCTTCAC TAGAAATTTT ATTGCCTAAA ATATTCTCAA TTAAACTAAT       1920
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TACAACTGCA ATATCACTAA ATTCTATATT TAAAGATTTG TCAAAAGATA ATGAATAAAG   1980

TTTAATTAAA GAAAATATTA TTCTTAAATT ATCTATATAT TTACTTTCTT CATATTCTTT   2040

GTATATCTTT TTAGATCTTT CTATATCTTC CTTAGTGGTA TCGTTAATAC CTTTAATTTT   2100

TTGATAACCA TCTTCTAAAA TAGTTGTAAT TTCCTTAATT CTTTTTTTAA ATAAAGAAAA   2160

TCCACTTTCA AATTTCTTTT TTGCAATATC AAAAAATTCA TCTTTAGTAT ATCCCAAGAG   2220

AGCATTTCCT GTTTTTATAT GATGCTCAAT AAAGCTTAGT GGCGTTCCAA AAATAAAGGT   2280

ATTAATCCAC AAACTTAGCA TAGTAATTTC AACCGAAATA GGAT   2324

(2) INFORMATION FOR SEQ ID NO: 56:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2148 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TnAAATCTAG GATACCCCGA cAAATATTAT TTTCCAGTAA TTATGAATAT TTGCTCGTAC   60

GACAATGTAA AGAAATTGCC TTATGACGAG CTTTTAGAGG TCAATAGACT TGCTGAGATT   120

AAATTAGAAA AAGAATTGTA TGAATTAATT TTAAGCAAGT GAGGGCTTAG TGAGCGACAA   180

ATTCACCATT AAATTTAAAG GGATTCTTGA TCATGCTGCA ACAAAAAAGG CCATTGAACA   240

AGATATTTCT AAAATGGAAA AATATCTTAA ACCCAGAAAC TCCAGTTTGG GAAGCACTAA   300

AGATATTGTA AAAAATAATT TGTCGrACAA GAAAAAAGAA CTTAGyArAC AATCTAAATT   360

TGAAAGCTTA AGAGAGCGTG TTGAGAAATA TAGACTTACA CAAACTAAAA ArCTTATAAA   420

ACAGGGCATG GGrTTTGAGA AAGCTAGAAA AGAGGCTTTC AGAAGATCTT TAATGTCTGA   480

TAGAGACAAA AGGCrTCTTG AGTATAAAGA ACTTGCAAAA GAATCAAAAG CAAAAAGTAA   540

AATGTTAGCG GCCTCTCAAG GAAAAGGACT TGTTGCCAAA ATTGCAATAG GTAGTGCCCT   600

ArGGAATATC ATTAGCAACG CTATGAGTAA AGTTGGAGGA GGCCTTTTAG GTTTTGCTAA   660

AAAAGCrGTT GAAGAAGACA CCAAAACAAA AAGAACAAAA CTTCTCAATA GTGCATTTTT   720

TACAGATAAC GAACGAAATA TGATTATGGG AAATAAAGAC AAGAATACTA AGGGAATTCT   780

TGACGGAATG AArGGwTTTG AGCGmGACTT AGAAAAAGAA GArTTcTtAm ATCAAGCAAG   840

TGyCTTTAAG GGTACTyTAA GGGACyTAGA TATGTTAAAT GAAACTAATT TGAAAAACGC   900·

aGTAGAATTT GCAGCTATGC TTAAATCCAG TGGTGCTATG AGCAGCGAAG ATGCAGTAAA   960

1037

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GGCTGTTAAT AGTGTTCTTG GGGGTGATGG AAGTGAGCTT TTtGATCTAT TAAAGAAGTC    1020

aGGTGTTGGA GACAAATATA TAGAAGATGC CAAAAkGGCy TGGCAArGCG GGGCwsArGT     1080

AGATCTAGAG TCyAGAATTA CCAAGATGAT GGAAATGTTC GAGGATTTTA AATCTTTCGG     1140

CCTTACAAAA AAAGTCAATA ATGCTGAGAG TATTCAAAGT AATTTGGCCT CAGCTGAGCA     1200

AACTCTTCAA AACTTAACCA CTACTGTCTT GGACCCATTA CTTGACCTCA TTAATAAGAT     1260

AACTAATTAC TTTAAAGACT TTGCGTTTGA AACACACATT ATTAATCCCA TAATTAATGG     1320

CATTAAAAGT ATTTTTAATC TTAATTATTT CTTTGCAAAA TTAAAATCGA TGCTACCTGG     1380

ATGGATGGGC GGAGATGAGG GTGCGGCTCT AAAAAAACTA CAAGAAGAAA TTCAAAATCA     1440

AGACAATGCT AACAGCACAC CATAATTTTT ACAAAGGTA ATTACTTATG ACAAGTAACA      1500

AAAAAATTGC TAACAATGCA GCTAACAAAA TAGATATTAA TAATAAAATT ACTAACAATC     1560

ATGATATTGA AAAGAAAAAA ATCAAGGAAA AAATyAATGA TATTGAAAAG AAAGAAATCA     1620

GGGAGATTAC TCGAATAATA AGAGATGTAA TAACCCAAAT ATTTGCCCTT TTCGGAGCAG     1680

ATAATTTTTT AGTGTTATTT CCTAGAATGG ATCTAAAAGG TTTTGGATAT ATTCCTCAAT     1740

TGTTTTTTAT AAAACCAAAA AATGAACTCA TAACACGCAC TTATAATACT AGTTGTTCTA     1800

AAAGACCAGT TATCAATTAT TATGATAGAA AAGCGGAATA TGTAAGCTAC AATCCGGTAA     1860

TGACTGGTGA ACATATCTCA TTAAACGGkG GAATACTAAC ATCCTTATAT AAGGATATGm     1920

TTTCTTTACT yAAAATGACT GTTTTTGGCA ATACTATGCT ACGTTTTGAC GCGCATCTTG     1980

TAAAAGAACA ACTAGCCAAT AGAATACAAG CACAAGTCCC TTTTAGTATm TATAGTCCAA     2040

CTTTTGGACT TAAAGAATTA GCTGTAATTA CAAGTCTTTC GTTTAAAGAT ACTCCTTTCA     2100

TTGACGAGTT GAAGGTTAGT CTGTCAATAG AAATAGTAAA AACATTCG                  2148
```

(2) INFORMATION FOR SEQ ID NO: 57:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2123 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
ACATATTATT TTGTTTATTT TTACTAATGC TAAACGGCTG TAATTCTAAT GATAATGACA      60

CTTTAAAAAA CAATGCCCAA CAAACAAAAA GCCGGAGAAA ACGTGATTTA ACCCAAAAAG      120

AAGTAACACA AGAAAAACCT AAATCTAAAG AAGAACTACT TAGAGAAAAG CTAAATGATG      180

ATCAAAAAAC ACAACTTGAC TGGTTAAAAA CCGCTTTAAC TGATGCTGGA GAATTTGATA      240
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AATTTTTAGA AAACAATGAA GATAAAATAA AATCTGCACT TGATCATATA AAAAGTGAAC          300

TTGATAAATG CAATGGAAAA GAAAATGGGG ATGTTCAGAA AAATACATTT AAACAAGTAG          360

TTCAGGGAGC TCTTAAAGGG GGAATAGATG GCTTTGGTGC AAGCAATGCA ACTACTACAT          420

GCAACGGTTC CTAATAGCTA TTAGCCCCCT ATTTGGGGGC TTTAATCTTG CTATGCTGCA          480

AATATCTCAT CAAACCGTTC GTATTCTTTT AAGATACTAA AGAATATTAA TGGACTAGGG          540

CCATAAATAG GCCTCTTAAG CCCCATAAAC CTTTCAAAAT CTTGTAAATC CTTTAATCTA          600

TTATTTTTCT TGAAATAGTT TTTTATAATC TCGGCCCAAT AGTTTATGCT TTTAAAATCA          660

CTATTTTTCT CAAAATACGA GATTAAATCA GATTCAATTT TCTTGATATC ATCAAAATTA          720

TTGGGGTCTA TATTCTGAAT AAAGCTTATT TTTTGAATAA TTGAGTTTAT ATTATCTTTT          780

GTTGTAGGGC TATTTACCCA GTCTTTTATA TTAGACAAAG CTTCTTTAAA AACACCGTAA          840

TAATAAAGCC TATCTTTTTT TTGTTCTTGC TTAATATCTC TTTTCTGGTT TTGAATAGTG          900

TTATTTTTTT GAATTTGATT AATCTCTTGT TTTTGTTCTC TTTTTTGTTC TTGCTTTTGA          960

TTAACACTAA CTTGCTTGCT AGGCATAGAA TTTTCGTTTT CGTGGTTATT GTAAATAGGA         1020

GCTGCATCAG TATCTATTTC ACTTTCTATA CCAAGAGCTG CAACTAAAGC ATACCTTTTG         1080

ACATAAGTAA TGCCTGAACC AAACATCTGA TACACTGTAT TTGTAACTTT AGACCCATTT         1140

TCATTGTTCC ATTGTAAATT TTCTGTAGGA ATTCGCGTAT CAAAAGAAAA TTCATATCCA         1200

GTACTTGTAC TGTAGAATGT AGTCCTAATA TAATCAACTA TGCCATATTG ACCCTCTATA         1260

GAAATTGGAT ATTGCTCAAT ATCAAGCTCC AAATTGTGCT TTTTAATAAC ATTTTTAATT         1320

TCTCTAACTA TTTCATTGAA ATTTTGATAT TTATATCCAT ATCCTTTAAG ACTTTTGTCA         1380

ATCCCTGGTA AATTCATTTT TAGGGTTTTC ATATCTTTTC GGAAGCTTAT TTTTGCTTGA         1440

ATATTATTTT GTATTCTTG ATTATTGTTT GAAAGATTTT CCATCTTTTT ACTCCTATGG         1500

TTATTTATAA AAATAAGTAT ATAGCAAAAA CTATTTTTGC CAACTTTTTT ACAAAAAATT         1560

TTACAAAAAA ATAGGGCTTA GCTAAATTCT CTATTATCTA CTAAAGAAAT TAGTTAAGCC         1620

CGTGCTAAAA ATTTTTTTGC AAATTACCAT AGGTAGTCAA AACTGAAAAA TGTTTAAATA         1680

ACTACGCTGT TTGTAGTGTA GCCCAATTTT AAATTAAAAT CAATTTATAT TTTCACTGAA         1740

TTAAAAATTT CTATATTAAT TTAACAAAAT TAATAATTAA AATTTAATAT TTTTTTAGAA         1800

AAGTATTTAC TTTTAAATCA AAATTTTGCA TTATAATAAT TAATTATTAA TTACCATAGG         1860

AGAAAAAACA TGAAAGGTTT TTCAAATACC ACAAAAAATC CCACTTGCCA CAACAAACAC         1920

CAACACAAGT TAATATATCT AGCTTCAACA CTAGATTTtC TAAACAAAAA AGaTAAGAAA         1980
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1039

TACACACAAC AAAACATACT CTATTACTAT AATGrrAATC TAAAAAGAAA TGGkCTAGCT   2040

CCCACTACTC TAAGrACmAT GgCAAAATTA TCTTTACAAA TTAGAAAAAG TATTAAAAGT   2100

CACAACTAAT TACTAACCCn AAA   2123

(2) INFORMATION FOR SEQ ID NO: 58:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2093 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

AAAAAAGTGC GCCGTGCGGC GGTGnAACGA CTCAATAGTT ACTAATAATC CATTTCTAAA   60

CTTAGAAATG CAAATTAATA ATATTTTCTA AAGTATTTTT TGTTTCCTCA TAATATGTTT   120

CTTTTACAGA AGGTTCTAAA AGTTCATTTA TAAGAACTTT TACACTATTG TAGTAATGAA   180

TTTTTCCCTT TATGTAAAAA GAATATTCCT TATAAAGCAG TTCTTCTACA TCTTTAAATG   240

TATTTCTATT TTTTAGAAAC TGATTTTCTA TAATCGAAAT ATTAAAGCTT TTATTTCTAA   300

AATCTTTAAT ATCATTAATG GTTTGCATTA AAATACTTAA ACTTTCTACA GAGAATCTTT   360

CTACTTGAAC TGGAATTATT ATATAATCTG TAACATTCAA AGAATTTTTT AAAATAAAAC   420

CCAAGTTGGG TGGGGTGTCA AGTAAGATAT AATCAAAATT ATAATTTGTA ATATTTCTAT   480

TCAAAATATT TTCTAAAAGA AGATCTTTAT AATTTAAAAT TTCTGAATTA AAATTTTCTA   540

AAATAGGATG AGATGGAATT ATAGAAATAA AATCATTAAT TTTATTAATA CACTGTCCAA   600

AATAAACATC TTTTTTTAAT AAGCTGTAAG AATTGCATTT ATCAATGTTG AAAATATATT   660

TACTAAAATA AGAACTTAAA GAATTCTGTG GATCTAAGTC AATCAATAGA ACTTTTTTGC   720

TTAAATCTTT TAATATATAA GAAAAAGTA TTGTTAATGT GGTTTTACCT ACACCTCCTT   780

TAGGGCTTGC AATTGTTATA ATGTTTGATT CTTTTCTATC CATTTGTTTA TTATTCCTTC   840

CTCTTTTATT TTTTTATTGT AAAATTCGTA AACTGTTTTT TCCATGTTTT TTATATTTTC   900

TAATGTAAAT TTATAGTATT TTGTTTGTTT TTTTTCTTTT CTTAGTAATG TCCATAGGGA   960

CTGAACGTAA CACTTAATAG ATCCTTTTTT AAATACATAT TCTATGTAAT ATGCCTTTTT   1020

TACTACATAT TTTATATTAT TATTGCCTAT GATAAAAAAA GGTTTCTCGA GATTATCCCA   1080

ACCGTATTTT ATGCCTAAAA ATTTTTCATC TTCTTTTATT GGAAATAGAT TGAAAAAATT   1140

CCATCCTCCA GTATCATTAA ATTTTTGGAA GGTTATCCTA AGACCCTTTC TAGTAATTTC   1200

AAATTTGATT AAATGCTTAA ATATTATTGA ATAATATGTT TTTTATTCT CCTTTTCTTC   1260

1040

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TATTTTATAA AAGAAGATTC TTTTTTTTGT TTTCTTTTTA AGATTTCTAA ATCTTTCTGT    1320

AAAGTTGTTC AAATTTTTTT CCTTTTATAA TTAGCTAGTA AATCAAATAG AAATGTTTTA    1380

TTTTGATTTA TTTTCCATTT ATTGATGTAA GTGTCTTTAA ATTCTCCTAC AATTTTGAAG    1440

AAATCTGTTT CGTAGTGAGC ATTTTGTCTC ATGAAGTGAA TTTTATTTTT ATATTTTTTT    1500

AGCTTTTTTA AGTAAAACTC TTTTATATCT TTTGTTTGAT AGTCGTATTT TAAATGCTTG    1560

TTGAAATCTT TGTAATTTAT AAATAACAAT GGGGTTATTA TCAAGGCTGG TGGTGGGCCA    1620

CCAACCGCAA TTAATGCATA TGCCCTCTCT GATTCATTTA CAATCAATTT TGCACCCGAA    1680

GATGAACATC AAGATCAAGC TAAACATCCC AAACAAGAGT ATTCTATTAA TTTGATAAAA    1740

GTTGCAATTT TTGGCAATAG AGGCCTTGAG AAAACAGTAA CACCTGAAGC TGGTGGTTAA    1800

GCCTTGGGCA ATAAAAGGAG TTAAACAAAT GGCAGACACA ACGCAATTAT TAAAAGATTA    1860

TCAAGATAAA CGAgTAAACT TGAAAAGTTT ATGAAAAATC CCCAGTATGA CGCTGGTTTG    1920

CTTAGCAATT CtGTAGAGTT TAGAGATAAA AACATACAAT TTTTTGCCTC TGGAGGCACT    1980

AGAACCAGCA AATTtGACAA aTTAGAAAAT CATCCATTTT CtGGGTATCC ATACmAGCGg    2040

GGaTAAAAAG AGTTATTCAA GAGGAAAAAG CTGATCAAAT TCACTATGGA ACC          2093
```

(2) INFORMATION FOR SEQ ID NO: 59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2019 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
GTCTTAGTCA TATTTTCATT AAGTCTTTTT GCTTATTCTT AGCAACCTCT AGCAAACTTT      60

TAGTACTACT CATTGAAGCT TTAGCATCAG CCATAAATTG GTGGTAGCCA GCATAGTAGT     120

AGCTCTCATG CCTTGAAGCA TTGCTATTAC TTAATGCCTC TTCTAAAGCC CGATCTGCTT     180

TTCTTTGTGC ATACTCAAAA TCGTTCTTAG CTCTTTTTAA AGCAGCAATA GCATCATTGC     240

AATGAGTATC AGCAGAAGCA TGATTACTCT TAACCTTAGC AATAGCTTCT TCTAGGCTAG     300

GCAATAAGGC TAAGTTAGCT TTACTAGATC CCACACCTCT TCTAGTCTGC TCTAAATAAG     360

ATTTAGCTGT ACTAAGTAAG CTTTTTATCT TATCAAGGCT TGCTTTTACT TTTGCTAAAT     420

CTTCATTTAT TCTATTGTAC TCTTCTTTAG AAGATTCAAT TTCCGTCATA ATGTTTCTAG     480

CTTCACTAGC TTCATTATCT TGGATATTAA CTTGTAGAGT ATGGTTGCTG CTACTATTAT     540
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1041

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CATTTTGCAT ATCGGGTTGC ATGTCTGCCA TCAAAGGTTT TTTGCCTGTA TCTTGGTCCA    600

TATAAGTATT ATCTACACTT CTAGGCTTAC GACCACTTCT CTTGCTGTCA TCGTTACTCT    660

TTAGAGTATT AAAAGACCCA TTATTGCTTT TTAGTTTGTC TATAACCTGA TCGGCGTTGT    720

ATGTAATCTT CTTGTATAAT TTACAAGAGA TAACACTGGA AAATAAAATA GTTAGAATAA    780

ATAATTTATT AATTAAATTC ACCTTATTAC TTCTCTTTAG AATCTGATAT TCTTATATTA    840

AAAAATATAT TGCATTTATA ATTTATAAAA TGATTAATAA TGCATAAGCC AAACTATAAA    900

TCTGAAAGAA TTAAAGTAGT GTTTGTAAAG GCAAGATAGG AGTGAGATAG TTAATTTAGG    960

TAAGCTGATA TAAGTTTTTC TAGTAAATAG AGTTTCATAT ATGATTAGAG ATATTAAAAA   1020

AACTAAAGCC TACACTGGAA GTTTTAAAGC TTTAATATAT TTTCTATTTC TTTTCTGCAA   1080

GAATTTCCAT ATTGAAGAAA ACTAATAGCA TTTTCCATAT ATTTAATGCA TTCAGTAGCA   1140

AGATCTATAG CTCTTTTTGC TAAATCTTGT ATATTGCGTT TGTTAAAATT ACTGCCTAAC   1200

CAGTATGAAT TGCCATTTTC ATTGTTTAAT CTTTTATAAA TAGAATCTGC TAGTTTATCT   1260

CGAGCCACAT CTAGCATATC TTTAGCAGAC CCCCAAGAAT TAGTTGCTTG CTCCATAAAA   1320

GAACGCATTT CTTCTAATTT TACCCATAGT GTGGCTTTGA CAGACTTTAT TTTTCTATTT   1380

AAAGGAGATG TGCTTAGATT AGAAAATAAT AAATCTGACA TTTTTTGATG AAATTCTTTA   1440

AACTCAAGGA GTGTATTGTT TAAGTTATTT TCAGAATTAG CACGATTAAT AAACTGCTCT   1500

GCATTTTTAA TTTCTGAAAG AGATGTTTGC TCATACTCTT CTTGTGCAAA TTCATCTAAT   1560

TTAGCTTTAA TTTCTTCTTC TGAAGGAATA GCAGGAGTTT TACTTGTTGT AGTAAGGCTA   1620

TTTTTAAAAT TACTTTGTTC AATTGGATCA TGTTGTGGAG TAGCTGATTT ATTTTCTTCC   1680

ATCTTTACAT TATTTTGAGC ATGCGAGTCA TTTTGCATTA TTGCTGGACT TGAATTTGGT   1740

AGGGATTCTT TATTATTTGC ACCAGGATCA TCTGACATAT GTTGATTAGA ACCTACTTGT   1800

AAGATTGGAT CATAAGTTTT TTTATTTGAT GATGTAACGT CTTTAGGAGA TTCAATTTCC   1860

TTACTATTTT TATCTACTGA AGTATTAGTA GTATTTTTAT TTTCTTGATG ATCTTTTAAT   1920

GCTAATGCAA ACTGTTCTAT AGATTTTTTA GATAGAAAC CAGAACAACT TTCAAATAAA   1980

AAAAGAGAAC TAAATACTAA ATTAGGTATA ATAAAAATT                          2019
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(2) INFORMATION FOR SEQ ID NO: 60:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1907 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

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AGAAAAACAA AATCTATTGC TTCTTCACTA AATCCTATCT TTAAAAATTC ATTTTTTATA        60

CTTTCTATAT TGTATGTTCT GTAAGTCAAA CTATTCATAA AATTTCCATA TTATCCTTTT       120

AATTCTTTAT ATTCTTTCAT AAGTTTTTTA ATTATTTCTT TTCCATCACT AAATAATTTA       180

TCTAACATAA ATCCTGTAAA TTTAGCATTA CTTTTATAAA AATCATAGCT TTCTTGTCTT       240

TTAAGCTGAA ATCTTAAGGG CTTTATCGGG TTTTGTTTTG ATTTTTTTAT TGTTTTGCTC       300

TCTTTATTTC TTAATACAAT TAACGTTTCC AGTATACCAT TTTTTATTAG AAATTCTTCT       360

TGTATAATCC CATCTTCTAT TGCATTAGCA ATTTTTAAGT AATTATAGAC CTGTGCTCTT       420

GCAAGTCTAT AATCTTTAGA AAAAGCTTCA AAACTTTTAT AACCATCAAA CCTATAATAA       480

TGATTGTCTT TAATTTCTTT TAAAATTTTT AAAGTTTCTA ACTTACAATA GATTTCCTTT       540

TTAGAATTAA TTTTTAACTT TTCTTTTAAA GAATTATAAT GATTTAATAC ACTATCAGTA       600

ATAATATAAT TTTCATTATC ACTTAAATCT CTTTTATTAA CCTTAATATC CAATTTAAAC       660

TCCTTTTACA TTAAACTGTC TAATTATTAG ACTTTATATT TTTTTAAAA AAATTTCTAA        720

AATATTTTCA TATTCTTTTA TATAATCTTT ATTTAAATCA AAATTATTAT TTTCTGCTAT       780

TCGTCTATTT AAGTCTTCTC TTTCAGATAT TGTTCCTAAA AATCTATCTT TTGTTTTTAA       840

TATTTCAAAT AATGTTTTAT GwGTTCTAkT TwwwtTaAAT CTTGTTATTA TCAAAAATAT       900

AGGTAAAAAT AAATTTAATT TTCTTACAAA GAAATTAAAT AAATCTAAAC TTTCCACTGC       960

CCACTTTTCA GCCGTCATTG GAATTATTAC ATAGTCACTA CATAAAGAG CATTTTTTAA       1020

CGTAACATCT AAACTGGGAT TTGTATCGAT TACTATATAG TCATATTTAT AATACAAAGT      1080

TCCCAGGCTG GTTTTTAACA AAAAATCTTT ATGTTCGATT TTATCTTCAC TAAAATTATG      1140

TAGCGTAAGA TAGCTAGGTA TAAGATCAAG ATTATTATCT ACATTTATAA TGGTACTATC      1200

GATATCTACA TTTTCTTTCA AAATCTCATA AATATTAAAT TTGGTAAAAT TAATACCTAG      1260

TTTTTCTATT TTTTCGTAAA AATAACTAGT AATAGATGCT TGAGTATCCA TATCAATTAA      1320

AAGAACTTTA TTATTTTTTG ATAATAAAGT AGCCAAAATT ATCGCACTTG TGCTTTTACC      1380

TACACCGCCC TTAATTGACG CTATTGTTAT TATTTTAGGT TTTTTATTAT CCATTTTATT      1440

AGTGGTCCTT GTTCCGGGTA TTTCTTCCCA TAAAATTTAT ATACTTGTTG TTCTAAATCT      1500

GTAAACATAC TAAATAACAC TTTGTTGTAG TGATTGTTTG TTCTTTTTTT ATCTAATAAA      1560

CGATATAATC CCTTGAAATA GCAAAAAACA CTTCCTGCTT TAAATCTAAA TTCCATATAA      1620

TATGCCCTTG CTAATGCATA TGCTTTTCTA GCCCCGTTTA TTTGATACTT TATTAACGGC      1680
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1043

TTTTTAATCG GCTTTCTATA GCCATAAAAA ATACCAATAA ATTTATCTCC TTCTTTAATT   1740

GGGTACAAAT GAGTTTCTTC AACAATTCTT TCTCCATTAA ATAAGGCCCT CAATGATAAT   1800

CTAAATTCGT GTTTTTTCTC ATAAACTCCA AATTTATAAA TATCCATCAT TATTTTTGTA   1860

TGGTACATTG CTTTACCATT TTCTTTTTCA ATTAAAATAA AGCGTTC   1907

(2) INFORMATION FOR SEQ ID NO: 61:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1907 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAAAAGATAT ACGTAGAAAT AGAAAGACGT ATTGAAAACC ACAATTTTTT GTTTTACAAA   60

GATGAATCTT TAGTACAACT ACAAGACGCA CTTTCTAGTG CAACAACTTC TTTAAGTGCA   120

CTTACTCAAG GCAATAATGA TAGAGGAAGT GGCATTTTAT CTTCTTTTTT AAGAAAACAA   180

AATTCAAACA ATCATAGTAA AGATATTTCT AATTTACGTA GTCTTAATGA CTCATTGGCA   240

CAGGAACTTG CTAGGTTAAA AAGCAATCTA AATAATGAGG GAATGTTTTA TACAGCTACT   300

CCGAGTGCTA GTTTAGAGGT TATTAAATAC GATCTTAGCT ATTTAAAGGA GGCTTTAGCA   360

TTAATTAAGG CAAAAATTGG TGCAGATACT AAAGAACCCC TAACTAGAAG TTTTAATGAG   420

CAGGCTAAAG GACTAGGGAA TGATGGTAAA GGAGATAGGA GCAATTATTA CGATTTTCTA   480

AAAGGTGTAC AAGAACAAGT TGAGAACTCT TGTAATTTAA AACTTACAAA GTATTTTGGA   540

CTTGATATGA AGTTTAATTC GCTGATTATG TTAAGTGAAG AACAAAAAGT GGAAAGAGAT   600

ATAAAGCTAA TTGAGCTTaC AGTAAATATA ACCAGCTTAT ACAAAGTAGC TCCTTgATAA   660

TGAGGAGTTA GCGATTTaAA AGAGAAATaT TCTCATTTtG AGAAAAGGAG TTAAAAAGTG   720

ACTGAGAAAG AAGAAAAAGA AGACCTGCAG GCACmAGATA AAGArGAGCa GCAAaTTAaG   780

GCtGATACTA AAGTTATAAG TGCGCAGGAA TTTGAAGAGT ACATGCGTTT TAAAGAGCAG   840

GCAAATAGTA AATCTAAAGA GACAAGTCGA GATTTAAGTA TAAATGAACG AATAACAAAA   900

GAACTTGCAG AAGTTGAAGA GCGGGAGCGT ATTGAAAAGC AATTGTTACT AGAGGCTGAG   960

CGAATTAATG AAATTGATAC ACTTGCAAAA GCACATCTTA GCAATCATTT TAACAAAGAG   1020

GTGCTACTTG CAAAAGGATA TACATTAAAA GACATTATGC AAGCACAACG TAGAGAACTT   1080

GTACGCAAGT TCGTTCCAAT TGAGCAAATT AAAGCTATTG CCAAAGTATC AGACATAAGT   1140

CATATmGATG GrGAGATATT AGAGCAACTT GTTTCTTTAG CAAAAGTGAA TATTAAATTA   1200

AGAAAAAATG CGAGTAGCAA TTCTTCTTCT GTTGACTCTA TTAAGGGGAA TATTGCTATT   1260

AAATCAGAAG AAAGAGCAAG TTTGCTTAAT TCTAATTTTG TACCTATTAA TTTCACAGAA   1320

TTTGTACAAG CGATAAGTAA TACTTACAAG CAAAGACGAA TTCAATTTTA TGAAAATCTA   1380

AAAAGACATA AAAGAACAAG TATTGCTTAA AGGAGTTTTT AATGAGCGAT GGTATTACAA   1440

AAATAAAAGA AGAGTTTGAT AAAAAAGTTG CAGAAATTAA AGCATTAATG AAAAATCCTC   1500

AGCAAGATrC TGGTTTGCTT AGTAATTCTr TAGATTTTAG AGATAAAAAT CTAATTTACT   1560

CCAATTCGGA TGGAGTTTTT ACTAGTAGTA AAGACAAAAT AGAAAATTAT CCTGCTAAAG   1620

GGTATCCATA CAAGCGTGGA GTCAAGCTTA GTTTAGTGC AGATGGTACA ACAGAACTAG   1680

AAGTTGAGGC TGGTGGTGGG GATGACTTGT ACGGAATATG CACTGATATA nATGAGTTTA   1740

CTGGCATGGC AACTGTAGTT CCAATTACAA ATAACTTCAC AGGGTATTTA ACATTTAAnA   1800

AAAATGGACA AAATGGTGTG AATCCGGGTG ATAAGCTGCA TTTTAATGCA CnAGGAGAGC   1860

TTGAAAAGAA TGGGGGAAAT GATAAATCTG TTAATGCTAT AGCnCTT   1907

(2) INFORMATION FOR SEQ ID NO: 62:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1902 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CGGGCATTTA AGCTCTTTTC TACATTGTCT ATTTTGATAT TCAAACCATC TATTTTTAAA   60

TTTAAATTCT TTTCCACATT GTCTATTTTG GCATCTAAAT TAGATATGTC TTTTTGCAAA   120

TTCTTCTCTA TATCAATTAT TTTCTCTTTT AAAAATTCAA AGTTGTAATT ATCATTATGC   180

AGAAAAACAA AATCTATTGC TTCCTtGCTA AACCCTATAT TTAAAAATTC GTTTTTTATA   240

CTTTCTATGT TATATGTTTT GTATGCTAAA TTGTTCATAG ATTATCCTTT TAATTGTTTA   300

TACATTTTTA AAAGTTTACT AATCAAATCT TTTTGATTTT CAAAAATCTC TTGCATCATA   360

AAACTTGTAA ATTTAGCATT GCTTTTGTAA AAATCATAAC TTTCTTGAGT TTTAAGTTGA   420

AATCTCAATG GTTTTATTGA GTTTTGTTTA GATTTTTTCA ATACTGGACT TTCTTTATCT   480

TTCAATACAC TTAATATTAA TCTAAATCCA TTATCTAATA CATATTGTTC CTCAATAACT   540

CCTGCTTCTA TTGCATTGGC AATTTTTAAA TAGTTATACG CTTGAGTTTT TGCAACATCA   600

TAATCCTTTA TAAAAGCATC GAAACTTTTG TATCCATCAA GTTTATAGTA TTCATTATCT   660

1045

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TTAATTTCTT TTAAGATTTT CATACATTCT ACTCTATTAG AAACTCCTTC TCTAAGGTTT      720

ACATACAATT TCTTTTTCAA AGTATTATAA CGATCTGTTT CAACACCATT TTTACTAACA      780

TTAGAAGAAT CTACAAGTAA TGCATTCCCC TCAGAATCAA TATCCCTTTT ATTGATTATT      840

AATTTTGTAT TATTTTTCAT AACAAGCCTC CTTAATTATA AGTTCAACGC GTCGAACTTA      900

TAATTATAAT TATTTTAATT TTGCATAAAA ATTCATTAAT GAATTTTTAT ACTCTTTTAT      960

ATAATCCATT TGAAAATCAA AAGAAGAATT ACTAGCAATT CTTCTATTTA AATCTTCTCT     1020

TTCTGATATC ATTCCTAAAA AATTTTCTTT GGAGTTCAGC ATTTCCAACA ATTGCTTATG     1080

TGTATTATTT TTTTTAAATC TCGTTATTAT AAAATAAGTA GGCAATTCTA CACCTATTTT     1140

TTCCATAAAA AATTTCAAAA GGTCAAAACT TTCAATTGTC CATTTTTCTG CTGTCAAGGG     1200

GACAATTACA TTGTTACAAC AAACTAAAGC ATTAGTTAAA GTAAAATCCA AACTTGGGGG     1260

AGTATCAATT ATAATAAAAT TATATCCAAC ATCTATATGT TTAAGCTCTT TTTTTAATCT     1320

AAATTCATCA AAAGTGTGCT TATAACCAAA AGCATTTATA CTATGTAAAG TCAAATAACT     1380

AGGTATTAAA TCTAAATTAT TCGCTACATT AACGATTGAT CGATTAATAT CTAATTTTTC     1440

TATTAAAACT TCATATATAT TATTTTTTCT TAAATCTATA CTGGATTTTT GTATATCATC     1500

ATAATAATAA CTAGTGGTGG ATGCTTGAGT ATCTATATCT ATTAATAATA CCTTATATTT     1560

TTGAGCCAAT AAGGTTGCAA ATATAATTGC ACTTGTGCTT TTACCAACAC CGCCCTTGAT     1620

TGACGCTATT GTTATTATTT TAGGTTTTTT ATTATCCATT TTATTAACGG TCCTTGTTCC     1680

GGGTATTTTT TCCCATAAAA TTTATACACT TGTTGTTCTA AATCCGTAAA CATACTAAAT     1740

AAAACTTTGT TGTAATGATT ATTTGTTCTT TTTTTATCTA ATAATCGATA TAATCCCTTG     1800

AAATAGCAAA AGACACTTCC GGCTTTAAAT CTAAATTCCA TATAATATGC CCTTGCTAAT     1860

GCATATGCnT TTCTAGCCCC GnTATTTGAA CTTATTAATG GC                        1902
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    (2) INFORMATION FOR SEQ ID NO: 63:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1761 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

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AACnGGCCCC GGAAGTTAAA GCCTTGTGGG nCCCATGCtC TAGTGGATGA CCGTTCTTTT       60

AGAGCCTAAA AAGCTATCAT GGGATGAAAC AAGAAGCTAT TTCTATAATC TTTGATTTAG      120

AAATAGCAGT TCACATAAAG ACGCTTGATA TTAATTTAAA TTTAATCTAT AATATAAATG      180
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GCGTAGTATG AATGTAAAAT AATTTACGTT TGAGCTGCCT TATGGAATCA TTTACAATTG   240

AAGGGCTTAA AGAAGTTCTT TAGCAAGAGA GTTTCTTTAA GCCCTAATAA TATTTGAACA   300

ATCTTTTTCT AGGTAAATTG ATCTTCAATA GGATTTTTTA AACGACAGTT GGAATCCGTT   360

TATTCCAATG TCAAAATTGG GTTCAACCCC CGCAAGTGCA ATGCCGAGCC TTTTTTTAAG   420

GTCTGCGTTG TATCTATTAG CAAATTTAAA TGGAATAATA ATTCCAGTTA TGTAGGATGC   480

TACAATTGTG AGCCCTCCTA TTCCTGATAA TACTCCTCCG GTTATTACTG TTGCTGTGCT   540

TTCTGTAACG CCTCCAATAC CTCCTACGAT CATGTGTCCA GCCATTATAA GTATTCCTTC   600

CAAGCACTTG AGAGCCAAGT AGTGCACCAC CACCAATATA ATCTCCTTGA ACAAAGATC   660

CTATCCCTAA AGACAAAAG ATATTCAAAA GTAATGGTGC TAGTATGGTT GCTTTTTCGC   720

TTTCATATTT CATTACAGTC GCGATATCTC CACTCCAACA CCTTTTTCAA GTTTATCTTG   780

TGCAAAGATT TGCATTGTTA AACTAAAAAT TAATATTAAT GTGAAAATTT TTTTCATATT   840

AATATTACCT CCTAATAATT AAGTTTTGAT AAACAAATGT TAGCACAATT TTTAGATTTT   900

ATTTATGGAG TTGAATCTTT TCTTAAAGAT ATTGTTTGAA TTTCTTTGCT GTTCTAAGCA   960

GATTTTAATG TAAAGTTTTC ATTAAACTCT TTTAAATTTG AAATTATGCT ATCTATTTTT   1020

TTTGTATGCC AATTGTATAA TGAATTGTTT TGATGACTTT TTCGAGATGT TCAACTTCTT   1080

TTGAGGGCAT TTCTCTGCCT TTTCTATAAG TTAAGTAACT TTTTAGAGTT TGCCAACTCC   1140

CAATAGTATA GTTATACACC TCTTTGGAAA CATTAATAAA TCTAGAAGTT TGGTTATAGT   1200

AAAGTTCATT TGTTTCTTCT TTATAAAAAA CTTTTTCTAT GATTGAGTTT TGTTTTAGGG   1260

TTTCATCTAA AAATGAAAAA CATTTTCCAA TGTTGATATT TATTGTTGGA ACAACTTTTA   1320

CTAAATGAGA ATTAATGAGA TCTGTTCCAA GTTTGCCAAG TGTTACAAAT ATGTCAGAAT   1380

TATCTACGAA AATAATTTTA GGAAAGTCTA TTTGTAGGTG TTCGTAGAAT CTATCTCGAT   1440

AGATATTTGA ATAAAGAATT GCGTAAATAT AGCCAAGTAT TTCTTCTGCA GTAAATTTTT   1500

TATTGTATTT AACATCAAGA AAATGTCTAA ATTTATTTTT AAAGTTTTCT TTTTTAACTC   1560

TCTCAGGTGT TTCGCTATCT TCTTGTATAT AAATTGGGAA AACATATCCT AGTGGAATAA   1620

TGCTTAATTC TGATATTTTA GAAGTAACGA AAGCATGAGA AAAACGATCA GTTTTGGATA   1680

GTCTTGTTGT TATTAGTGCT ATATTATTTT GAATTCTAA GATATGTTTC ATTATTTTAT   1740

AACCAGGCCT AATTATGACC C   1761

(2) INFORMATION FOR SEQ ID NO: 64:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1717 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

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GCATCATTTC TGAGACTGTT GTTTTTGTAG ATAAAAATTT TCCCAAATAA TATTTAAGCA       60

ATACAAGATT TAGTAAAGCG TATATTTTTA TTTTTTGATT TAATTTCAGT TATTTTTAGG      120

ATTTTTATTA TTTTAATCAT ATTTTCTTTA TCAATATTTA ATGTTAATAA AATTGAAATA      180

ATTTCTTTAC ATAAAAAGTC ACATTTATTG AAATGCTTTA TTACTTGATA CTTTTCTATT      240

TCGTTAATTT TTCTTTCTTC TTTTATATTA TTATTACAAT CTCCAATTG TACACTACCC       300

ATTTTTGTAT CAGAATTTTT ATTAAAATAG TTGGCAACTC TATTTTGAAA TCTTTTTTCT      360

TTTTTTTCTT TAAAGTGTTG GTTTATCTTA TGGTAACAAT CTTTTTTAGG ATAATTAAGC      420

TTATAATAAA TTTCTGTACC CGAATTTACC CCCATATGTT GATAGTAATT TGTTGTGACT      480

TTTATTTCTT TTTGTAGTCT ATAAATATAC TTTTGCATAG TTCTTAGTGT AGAAATAGTT      540

TGCCCGTTTT TTATAGATTT TCATTGAAAT AATATAATAT GGTTTTTGGG GTATATTTTA      600

GATTTTTGGT ATTTAAATAG CTTGTAGAAA TAAGAACTAT CAATTTATAT TTATATTGGT      660

TATAATTTAG AATATTACTA GATTAATATA TCTAGACTTT ATTTTCTATT TAATATACAA      720

TTAATTAGGA AGCATTATGT GCTCCAAATG GATGATAACC AGATAAAGGG CTTTAAGTGG      780

CTTAAGGAAG ATAAGTTACT TAAAGCCCTT ATCGCATTTA TACTAATTTC CCTAATTTAC      840

GTTTTATTTT GTTTAGAGCG TTATATTATT AATTTTTAAT CATAAAATGG AGGATTAGTT      900

TTGTAATTGT ATATATTTTT AGCTTTAATT GTTCTTTATT AGGCCTTTAA TACTCTAAAG      960

TATTATGCTA TTTCGCAAAA ATAATTTTCT GGATTATATT AGCTTACATA TTAGGATGAG     1020

AATTATAAAT TTTAGTGCAA CAACCTTCTA CAGGGTAAAG GAGTGTATAA AGGCCTCTAA     1080

AGCTTTCATT TTCTTTATTT GTGGAACATT TGAAGATTAC TTTTGGATTT TTTCTAATAT     1140

TTCAAGATAT TCTAACAGGG TTTTAGAATC AACTTCATGT TGATTAGTTT TAGCTAGAGC     1200

CTTATTAAAC TTGCTTCTTA TTAAGGAATA AGCATAATTT TTATTTGCAC TATGGAATAA     1260

TTTTTTATTC ATATGATCTA GTGTTTTGAC AAGAATGATT AACTTATTCT TAGCAAATTA     1320

AATTTGCTTT GTTATTCTTG CCAATGTATT GTTAATTACT CCATCCATAA TGAATTAGCC     1380

CCCTATTATA TTAAATTTAT ATTATAAATA TAGCACAGTA TTTTTTTAAA TTTTTTTAGC     1440

GTAAACAAT ATATTTCTAA AGTTTTGCAT AAGCTTATTT TATAATGTAT TTATAATTAA      1500

GTAGTAGTGA TTTTTTGTAA AAATTGTTTT AATTCTTCAT AGAATAATAC GTAGTAGTCT     1560
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TTTATTTTTA ATAAAACTCT TtCTAAGGAG CAATTAACTT TATAATAAAT TATAGATTTA   1620

GGATTTTTCT TAAAATAAAG TTTGACTATG ACGGTTATTT CTTTTTCTAA TTTGCGTTTT   1680

ATTTATATAT TTTTTAGTTT TAATTGTTCT TTATTAG   1717

(2) INFORMATION FOR SEQ ID NO: 65:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1566 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGnCACGTAA AATAACTTCA GTTCATATTA TCATATAATA AATAAAACAT TAAGTACAAT   60

AACCTAACAT TTAAAAAGGA TGTACATTTT AATACAGAAA CTGAAGCTGT TCAACTACAA   120

TTATTGCACT TGAAATTTTT TATATTTAAA TAATAATACA AATAATTATA TTAACAAATA   180

TCAATTAAAT TTATTTTTAC ATCATATAAT AGTGCTATAT ATTGTATAAT ATGCTATATA   240

CTTGAAACTA AAGGGGGGGC ATATTAGTTA AGATAATATT CTTATATTTT TTATTAAGGA   300

GACTAATATG AAAAAAATAT CAAGTGCAAT TTTTACAATA ACTTTTCTTG TTCTTATCAA   360

CTGTAAAAGC GATACTAGAA AAGCTATTAA TTCAATACAA ATCCAAAAAT TTACTTCCTT   420

TGATGGGTTG ATTGATGGCT TTCTACGCCT TAATTCAAAT CCCAAAAAAT CTGAGAGGTA   480

AAAGATTGTT TTAACAGCAT GGCTAAAACA TTAAATAAGG CCAAAGACAA ACTTGCTAAA   540

TTCATTAGTG AAAAAGGTGG CAAGACAACC GAAGGAAAGA ATACTGATAC TGCTAAAGAA   600

GATAATAGCA CAGTAAACCC TATTGATGAT GAAATAAGTA AAATTAACGA TATGATGGGA   660

AAAATGATAG ATGCTGCTAA TACCATTGTT GAAAATGTAG CCGAAACCGT AACTGAAGCT   720

aTGGGAGAAG TTGTCGAGGT TAAGAGTATT GGTAATGTAG CAACCAAAGC CGATGTAAAA   780

AGTGTTGTTG AGATTGCTAA AGGAATAAAG AAGATTATTG AAGCTGCTGG TATTGCCGAT   840

AAATTAAAAG CTGAAGCCGA TAAATCTACA AAGCCAATCA GCGAAGAAAG TAACAACAAG   900

TAAGCGGGCA AGATGTTCTC TGGGAAGCAG GGTGATCAAG GTGGTCGAGT TTTCGATGAA   960

GTCATTCCAC CTGAGATTGG AAGAGGAGCT AATCCATTTG ATATTAAAAA GGCTACTAAA   1020

GCTATTGAAA GTGTTAGTGG AGAGCAGATA TTAGGATCTA TTGTTGTGCT GCTACTAAAA   1080

CCGTTAAAAG TGGTGGTGAG GAGCCAAAGG GGAAGAATGC GGATGAAGCT ACAAATCCGA   1140

TTGAAGCTGC CATTGGAGGA AATGACGATT CGGATGCTAC TGCATTCAAG GGGAATATGG   1200

1049

AAAAAGATAA TCAGATTGCT GCTGCTATTG TTTTGAGAGG AATGGCTAAG AACGGGGAAT   1260

TTGCTGTGAA AATGGGTCGA AAACCAAGTG GTGATGGTGA TAATATTAGA GTTCTTGTTA   1320

ATAATGCTGC TAATAAAACT GTTGATGCTT TATCTAAGTT AGCACTAGAA GCTATTAATG   1380

AAAGCTTAAC AAAAATAGCC AAGACTATAC ATTGAAAAAA TAAAGTAAGA ATCAGCATTT   1440

TTAATAAATA ATATTATTTA TTAAAAAATG CTGATTCTTA CTCAACATCT TACGTCAGTA   1500

GTTTACTAAA CTGCATAATC ATTACATATA CACCAACATA TCTAAATTTG CAAACAATCA   1560

TCTTAG   1566

(2) INFORMATION FOR SEQ ID NO: 66:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1552 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CTGTTTTGTA AACCAAAAGT GGATTATAAT AATTGGGCCT ACTAGCTTGA ATTCTAGAGT   60

CAAGCAAACT TACACTAATT GTATCTTGCG GCAATTTTGT ATTCCTCCTT TAAAATTTCA   120

ATTGCTTTTA CACTAGCATT AAATGCTATA GATGCACTGT ATGCATGGTT GCTATATTTT   180

GTGCCTAAAT TAATAAGCCC AACTGTTTGC ATATTAGATA TTGGATAAAT GTAAAAGTTA   240

ACTTTACTAA TATATTCGGG TTGGGATTGA CTTTCTAAAG TATACTTATG GGCTTTATTG   300

TGTAGAAAAT TGCTAAGCAT ACCATAAAGC ATTAACATAC GTGAATTAGC GTCAAAATCT   360

TGAGCGTTTA ACACTATAGC AATAATATAT ATTTGAAAAT TTAAACTGAA TTCCAAAGCA   420

TTTTCATAAA ATGCACCGGC TCTAGAATTA TGATCAAATA GATTTTCTGT ACCATCAAAT   480

TTCAATGCTA TTATATTTGA GCTAGCAGCT GTGATTTTTG AAAGGTACGG GTGATTGTAA   540

GTATTTATGA TATCGCACTC AAAATTATTT TCAGTTGCAT ACGCCTTAAA CCCTTTGAAT   600

ATTTGAGTTA AATGGTTTAA AACCATATCT AAAGTAAAAA TCATTCAAGT GTTACCTTAT   660

AAGTAATCTC GGATAACATT TTGGCTGTAT CAACAAGTGG AATTGCTGCG GTGTTACTAC   720

CCTTTTTAAA CTTACTTTTG ATTGTATTAG CCTTTAAGGC TGGAGAGACT TGTGCTGATA   780

ATAGATAATT TCCATAGTAC CTTATAAAAG CTTGTCCAAT AGCCTCCATT CCCGATTTGG   840

GGTCAAGATT AAACTTAGAA TTTATATAAC TATTATTGAT ATATTCTCTA AATTCAGAAC   900

TACCAGCAAT TTTGGTTAAA TGTTTTCTTG CTGGTAAATT GCTACCCCCT TTTTCATGCA   960

TTCTAGCAAT CCCTGCACGA CCACCAAACC ACCCAATTTC CAATTCCATT TTAAACTCTA   1020

GTTTGTCCAT ATAAACTCCT TTAAAACCAA AGTAAAATAT CCGATTGAAG AGTCAATACT   1080

AAATATTTCA AAGTAAATTA AATCCGAAAT TGATATGCGG TCTTTTAGTT CATAGTTAAG   1140

GTCTTGATAT GTGTAAAGTT TGGAATATCC TTGAATATCA GACATATCAG AGTCATAAAG   1200

CACTGCAAGT TCTTGTGGCC TTATGTCAAT AATAACTCCT GCAAATTCAG TGTACTTATT   1260

TTTATCAAAA ACTCTCTGAT AAGAAGAATC GTTTTCAAGT TTAACAACAG TGCCTTTATA   1320

AAACCTTAAA GGTTGAGGAT CCTTAAATAC GTTGATCATG cGGAAAGACA TATCTGAAAG   1380

TCTTTTTCTA ACACCATTCA TTAGACAACC CCCACACAAG ATGGCGTTGA AGTTTCTCTT   1440

TTTAGTTTTT CTAAAAAgCa TCAAGTTGTG AACAAAAATT CyTGkTTGAG CCACAACCCC   1500

CCTCGsCGGC TTCTTCGGCT CCACTGGCTA CTAGGnTAAT AATCAAGTTC CA   1552

(2) INFORMATION FOR SEQ ID NO: 67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1484 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AGTCATTACC GGATTGTAGC TTACATATTC CGCTTTTCTA TCATAATAAT TGATAACTGG   60

TCTTTTAGAA CAACTAGTAT TATAAGTGCG TGTTATGAGT TCATTTTTTG GTTTTATAAA   120

AAACAATTGA GGAATATATC CAAAACCTTT TAGATCCATT CTAGGAAATA ACACTAAAAA   180

ATTATCTGCT CCAAAAAGAG CAAATATTTG GGTTATTACA TCTCTTATTA TTCGAGTAAT   240

TTCCCTGATT TCTTTCTTTT CAATATCATT AATTTTTTCC TTGATTTTTT TCTTTTCAAT   300

ATCATGATTG TTAGTAATTT TATTATTAAT ATCTATTTTG TTAGCTGCAT TGTTAGCAAT   360

TTTTTTGTTA CTTGTCATAA GTAATTACCT TTTACCAAAA TTATGGAGTG TTGTTAGCAT   420

TGTCTTGATT CTCAGCCTGT TCTTGCAGTT TTTTTAAAGc TTCGCCGCCA TCTCCGCCGA   480

ACATTGTAGG TAGAACCGAT TTTAATTTGG CAAAGAAATA ATTAAGATTA AAAATACTTT   540

TAATGCCATT AATTATGGGA TTGATAATAT CTTTGGTAAA ATCAAAATTT TTAATTTTAG   600

CGGTGATCCA GTTAATGATA TTAAGTAATG GGTCCAAAAC AGTAGTGGTC AAATTTGAAA   660

GAGTTTGCTC AGCTGAGGCC AAATTACTTT GAATACTCTC AGCATTATTG ACTTTTTTTG   720

TAAGGCCGAA AGATTTAAAA TCCTCGAACA TTTCCATCAT CTTGGTAATT CTGGAATCTA   780

GATCTACCTC AGCCCCGCCT TGCCAAGCCC TTTTGGCATC TTCTATATAT TTGTCTCCAA   840

CACCTGACTT CTTTAATAGA TTAAAAAGCT CACTTCCATC ACCCCCAAGA ACACTATTAA   900

CAGCCTTTAC TGCATCTTCG CTGCTCATAG CACCACTGGA TTTAAGCATA GCTGCAAATT   960

CTAyGCGTTT TTCAAATTAG TTTCATTTAA CATATCTArG TCCCTTArAG TACCCTTAAA   1020

GrCACTTGCT TGATTTAAGA ATTCTTCTTT TTCTAGGTCG CGCTCAAATC CCTTCATTCC   1080

GCCAATAATC TTTAAAAGAC TCTCTTTCTC TTTTGGATCA CCATAAAACG CTTTATTGAG   1140

AAGTTGTGTT CTTTTTGTTT TGGTGTCTTC TTCAACCGAT TTTTTAGCAA AACCTAAAAG   1200

GCCTCCTCCA ACTTTACTCA TAGCGTTGCT AATGATATTC CCTAGGGCAC TACCTATAGC   1260

AATTTTGGCA ACAAGTCCTT TTCCTTGAGA GGCCGCTAAC ATTTTACTTT TTGCTTTTGA   1320

TTCTTTTGCA AGTTCTTTAT ACTCAAGACG CCTTTTGTCT CTATCAGACA TTAAAGATCT   1380

TCTGAAAGCC TCTTTTCTAG CTTTCTCAAA CCCCATGCCC TGTTTTATAA GTTTTTTAGT   1440

TTGTGTAAGT CTATATTTCT CAACACGCTG GGTACCGAGC TCnA   1484

(2) INFORMATION FOR SEQ ID NO: 68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1452 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTGCTTATTA ATTCCAATAA GTGCTTATAA GTGTTGTTTT TCTTAAAATT AGTTACCATT   60

GGGAAAATCG GTATTTTCAA TTTTAATCTT TTTAGAGCAA ATTCTAATAA TTGCATGCTT   120

TCTACCGACC ATTTTTGAGC AGTCATTGGA ATTATTATAT AATTACTTAC AACTAATACG   180

TTTGTTAAAA TAATTCCCAA ACTAGGACTA GTATCTATTA TTATGTAGTC GTATTTATGT   240

TTTAATAATT TTAAACTATC TTTTAATCTT GTTTCTTTAA ACGGGATGTT ATCGTCATAA   300

AAAAGGTATA AATATATATA ACTGGGCAAT ATGTATAAAT TATTGTTTAA TCTAAAGGTG   360

GAAGAATTTA TGTTTTTTTT ATCTGCTAAT ACTTCGTAAA TGTTTTGTTT TGAAACATCT   420

ACCCCTTGTT CTTCCAAGAG ATCTGAAAAA TAGCTAGTGG TTGATGCTTG TGGATCGGCG   480

TCAATTAGAA GAACTTTATA TTTTTTAGAC AAGAGTGTTG AAAAAATAAT AGCACTTGTG   540

CTTTTGCCAA CACCTCCTTT AATTGAGCAA ATGGCAACTA TTTTAGTGTT TTCTCTATCC   600

ATTTATTTAT AATTCCTCCA TCAGGCAATT CTTTGCAATA AAATTCATAC ACTTTTTTTT   660

CCAATCTGTT TAACATGTCA ATAAATGTTT GAAAATATTT TTTATTAATT TTTTCTTTTT   720

TGATTAACCT AGCAAGACTT CTTAAATAAC AAAACACACT GCCTTTTTTA AATTTAAATT   780

CTATATAATA TACTTTGGAA AATGTATATG ATTTTAAAGT GCCATTGATT TTGTATTTTA 840

TAACAATGTT TTTTATAGGT TTTCTGTATC CATAGAAAAT TCCTATAAAT TTATCATTTT 900

CTTTTGTAGA GAATAAATTA AGTCCTTCTA ATTTTCCTTG ATTAAATAAT TTTCTAAAAA 960

GAATTAAAAA TTTGTTTTTT TTATATCTGT TTATTTCAAA TTTGTATAGA TCCATTAGCA 1020

TTTTAGTGTG ATATATTGCT CTTTCGTTGA GAATTCTTTT TTTGATGAAA ATTTCTGGCT 1080

TTCTACTTTT TTTTATTATT TCTTTTTTTT TGTTTTTAAG TTTTTCTAGT ACACTTTTCA 1140

TTTCAAACTC TTAATTTATA TAGCTATTTT TATAAATATT TTGTGATTCT ATTAGTTTGA 1200

TAATTTCATT ATAGTATTGA TTATTAAATA TTTTTTTGTA TTCAAGTTTA TTTTGTTTGT 1260

TTAAGTATTC TTTAATTTTC GACCTTAAAT TTGTTGTGTT GGTTTTTCTA TGTAATTGAT 1320

CTAAAAGTAT GTTATATATA TTGGTTTCTA TATTGTCTTT ATGTTTTTGG GGTTCGGTTT 1380

TATTAGTATC GTCCTTTATC TTTTTTATAA TTTGATCGAA ATCCGGGGAT CCTCTAGAGT 1440

CGACCTGCAG GC 1452

(2) INFORMATION FOR SEQ ID NO: 69:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1426 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC 60

TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT 120

TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG 180

CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT 240

TAGCTCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG 300

GTTATGGCAG CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG 360

ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT 420

TGCCCGGCGT CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC 480

ATTGGAAAAC GTTCTTCGGG GCGAAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT 540

TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTTACTTT CACCAGCGTT 600

TCTGGGTGAG CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG 660

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AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT    720

TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG    780

CGCACATTTC CCCGAAAGT  GCCACCTGAC GTCTAAGAAA CCATTATTAT CATGACATTA    840

ACCTATAAAA ATAGGCGTAT CACGAGGCCC TTTCGTCTCG CGCGTTTCGG TGATGACGGT    900

GAAAACCTCT GACACATGCA GCTCCCGGAG ACGGTCACAG CTTGTCTGTA AGCGGATGCC    960

GGGAGCAGAC AAGCCCGTCA GGGCGCGTCA GCGGGTGTTG GCGGGTGTCG GGGCTGGCTT   1020

AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC ATATGCGGTG TGAAATACCG   1080

CACAGATGCG TAAGGAGAAA ATACCGCATC AGGCGCCATT CGCCATTCAG GctGCGCAAC   1140

TGTTGGGAAG GGCGATCGGT GCGGGCCTCT TCGCTATTAC GCCAGCTGGC GAAAGGGGGA   1200

TGTGCTGCAA GGCGATTAAG TTGGGTAACG CCAGGGTTTT CCCAGTCACG ACGTTGTAAA   1260

ACGACGGCCA GTGCCAAGCT TGCATGCCTG CAGGTCGACT CTAGAGGATC CCCaGAtGGG   1320

GTTATTATTG TTACTGTTAA TGACTATCTT GCAGAACGTG ATTCCAATTG GATGAAAGCC   1380

GGTTTTTGAA TCTTGTGGGG TGTTAGCGTn GGGGTTGTTC TAATCn               1426
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(2) INFORMATION FOR SEQ ID NO: 70:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1425 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

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TTTTGGTTGn AATTGCCACn ATAAAAGGGA TTCTTTTTTG GGTTTTATGG GCGGTATTCT     60

TCATTAtAAA nTTmnTCtAT ACAGCAAATA TGGAAAGACT TGAGAGTGCA TTAACCCCAG    120

CAATAAATGC GGCACTCGCT CCATTAAATG AAAAAATCAA TCAATGCATT GACTTAGTTA    180

ATTCTGATGA AAAAAATCTC AAAATATCTA ATGATCTGAA ATTCAATCAG GAAGGAAAAC    240

CTATCTATAA GGAAAGAAyA AATAATGCAA AATAACACTA TTGGTTTAGG ACTTAATTTA    300

CTATCCAGCT TAACTAACAT AGCTAAAACT GATACAAACA TAGATCATAA TTACATTAAT    360

ACTTTTAGTA AAGTAATAGA TTTTTTCTAC AAAACATATA TAAGCACACT AAAATCTATG    420

GAAACAGCTG AGTCAACTAA AATATTTGAA GAAATACAAG ACATTTTAAA ATACAACATT    480

GAGATAATAG AGGCTATCTC TACTGATAAA AGCAAAGAA TTATCACTTC ACTTAAAGCA    540

ACACGTAACA AAATCATGAA AGAATATATC AAAATACTTA AAAGAGGTGA AAATGCTTAA    600

AAGATTGcAT TGTCTACTAA TTGCTTTGCT GCTATGTTGC ACCACTATTG CTAACCTACC    660
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AGAAGAGCCA AAACCGCCAA TTATTCAAAC ACTAAAATCT TTAGCTAAAT ATGAAACACA        720

ACTTTCAGAG TATGTTATGT ACCTTGTAAC ATTTTTAGCT AAAACAAAAG TCAAAGTTAA        780

TGACCCAAAT TATCCAGAAT ATCCTTATCC AGACTTATCA ACACTAAAAG ACGAACACTC        840

CATAACTGCA GTAAAACACA ATATCAACAT ATATTTAGAG TACATTAAAA AAACAAAACC        900

AATAGCGGAA AAAGTCTATA ATAAATATTC CCAATTAAAA ATGTAAATTA CAAAAAGGTT        960

TTTCTTGCAA GAAATTCTAC TTTATAATTA AATTGGCTTT TACAACAGAA GAAAATCTAG       1020

ATATTAAATT TACTTTAATC TAATATCTAG ATTTTAACAT TTTCAACATG AATATTTACT       1080

AATTAATTAG TGCCcTCTTC GAGGAACTTT ATTACTTTGT CTATCTGTTC TACAGCGTTT       1140

TTAGACATTT TATCCCCATT ACCAGAAGTA TTGCTTcCAA GAAGTGGTAC AGTTACTCCA       1200

ACTAATTTTG CTTCTGACCA TATTTTTCTT TTTGAAATAT CCTGATCCTT GTCAGTAATG       1260

TTTTCAATGG TATTTTTAGC TGCTTTTAAC GCTGCTAATT TGGCCGCTAA TTTATCCTGA       1320

AAGGAATTTT GCAAATTTAA TAGTTTTTCT TTAAGCTCTG CATTGCCTAT ATCTTTTAAA       1380

TTTTCTTTTA ATTCATTTAT TTTGTCTTTA TAATCTTTAA ATTTG                       1425
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(2) INFORMATION FOR SEQ ID NO: 71:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1423 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

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CAGGTCGACT CTAGAGGATC CCCTAAAATA ATTAACCCTG TCAATAAAGC GAGAGTGGAC         60

ATTGATTGGA TGATCTATTA CAGAAACCCC ATTAATATAC ACCTTTTTAA ATACAATCTC        120

TGTGTTATTT ATAACTTGTA TATTAAAACC TAAATCCATG TATCCGTCGT GATCATACCT        180

CAAAGTAAAA GATCCAAATT TGGTTTTTAA TTTAAGAATT AAACCGAAAT CATATCTATT        240

ACTATCATTT AAAATAACAA CTTCTTCAGA TATTTCACTA GGAAAAATAA ACCTGCTGGG        300

AATTAATAAA AAAGAAATTA ACAATATTAT TACTTTCATA CCTTTTATTA TTATACTATT        360

CTAAAGAAGA AATAAATAGA ATAAAAAATT TTAATTTCTC TTTTTTAAAA CTATTATTTC        420

TAGGTCAAAG ATTATAGAAT AGAAATAGTT TATTGCTTTA TCTAATGATA GCAGCTTATA        480

GGATCTTTTT TAAGATCGGT CTATCATCAA GAATATAAAT CACAAAGCT TTTTAAAAGC         540

TATCTAAATT CTTTATTCAA GGCAATAATT TATGTAAAAA TAATTAAAAA AACCTCCATT        600
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TTTGAGCAAA CATTTATACG AATTGATTTG GAAAGTCAAA TGCACAATTC TAACACTGAT   660

TGATAAAAAT ACTTTTTAAG TTTTTTATAT TCAAAATATA AAAAACTTAT TTATAAAAGA   720

TTTTTCAATA TCGATTTTTT TGTGATTTTA TTATTATTGG TATAAAATCA CATAGGGCCT   780

AACCATAAAT ACTCTTAAAG CAAGAATACT TATCTTAAGC CCTATAAATA GACATCGACC   840

AAAGTTAAGG ATGCTTATAG TTAATAGCAC CACTTACCAA GATTATACGC TATTATAGTG   900

TTAAAATCAA TACATTATTC TCAAATAATA TACATATTTA TTTATAAATT ATCTTTTAAA   960

AAATTTACTT CACTTTATTG ATTATTTTTC TAACACTTTC TGATTAAAGT CAATATTTTA   1020

CAAAGTATTT AAATTCGGGT ATTTGATAAA AATAGTGAAT TTAAATACTT TATTTTCCAA   1080

AAACTATAAT TTTATATTCT GCACACAAAA TTATCTATAT TAAATTTTTA ATTATATTTT   1140

TTACACTCCT TATATTCTTT CATAATTTCA TTAAGCAATT CTTCTTTATC TTTAAGTAAT   1200

TTTTCTAGCA AAAAACTAGT AAATCTTGCT TTTGATTGT AATATATGTA TGCATCTTCT   1260

GTTTTAAGCT GAAATCTTAA TGGCCTGATA AAATTTCGAT TGGATTTTTT AACTTTCCCC   1320

CCTTCTTTAT CCTTTAAAAA AAATAAAGAA TTCTGTATAC CGTTTTCGAT TATGTATTTT   1380

TCCTGAACTA ACCCTTCTTC TATTGCATTT GCCATTCTTA AAT   1423

(2) INFORMATION FOR SEQ ID NO: 72:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1405 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TATTTATnAA TATTGAGAAT ATTATCTAAT AAAATATTAA AGATGTAAAA ATTAGTTACA   60

AAAAATTGCT GTAGTGACAT AAATAATAAA ATTGAACTGC TAGAATTTTA TACAAAAAAT   120

AACAAAAACT TTATAAAGTT GATAATTATA AAAAATTTTA AGATTTTCTT GAAAAGTTTA   180

TCATATATAT AAAAAAAGAC AAGCACCATT ATTAATGTTT ATTAGTATAA AACCCCAAAA   240

TAATACAAAT TTAATCCCAA CAATATAGAT AGGATCTTAT TTTTTAGATA AAGTTTTTTA   300

AAACTTTAAA AAATATATTA AAATTTATAA AATATAAAAA GCCTATAATA CCGCACTTTT   360

ATTATCAAAA ATTGCTTATT TAATCTCATA AAAGCATCTT ATTGTTCTAT CAAGCTTATG   420

TATTCTCTAT TATAAGAGCA CAATTAATTA TACCAATTGG GGAGAATATT TTTATGAAAA   480

ACAAAATGAT TTTCTGTATC TGTGTTTTTT TACTTTTAAG CTGCTGTGCT GCAACCATGA   540

CACTGAAACA AAAATTGTTG ATAAAACAAA AACCTAATAT ATTAATGAGA TAAAAATTTA   600

ATAGCAGCAA GTAAAGAAAT CATCGAGAAA CGAACACTGC AACAAACTGA GCCAACAGAT   660

CAAGAACCTG TAGATAATAA AAACTGGGAG GAAGTTTTTG ATATAAATAA AAAAACTTAT   720

GACTTTATAA ATAGTTTTTT AACAAATGCT GAGTTCAATA TATTTGCAAC AATATTAAAT   780

AAACCAAAAC AATCACCAAG CAAGATGTTA AATAACATAG CAATTTTAGA GCTTAATCTG   840

GAAGAGACAA TTAATTACTT AGACTCAAAA AAAGATGTCT TAGATAAGGT AAACACCTTA   900

GATTTGGAAA AGATCAAAAA CTCTCTTGAA TAATTACTCT CTATAAGGAA TTTTTTTCAA   960

TAAGCATAAG AAAAACTTTA TTAGATCATC AAAATAATAC CGGTTCTATA AAAAAGGATT   1020

ATTCTAAATT AGATTCTTAT CTTAATACAA TACTTAATCA GTTAATGAA AAAATTAAAG   1080

AGGTTGGAAA TTTGAAAAAA ATTATATTAT CAATAACTGT TTCAGCATTA TAAATTAAAA   1140

TTTATTAATG CAGGGGCTTA AAGTAAATTA AACCTTTAGA TATAAGGGGC TAATAAACTT   1200

TTTTATTAGC CCCTGTTAAC ATTCCTTTAA TCAAAAATAT TGAATTTTAA TTACAAAAAC   1260

AAAAAAACAA TTAGATTGTG AAAACAATAA AGATCTTATA TAAACAGATA TCAATGAGCT   1320

TAAATCCTAT GTAAGTAAAC TTGCCGATGA TTTAAACAAC TATCTGCAGA AGCAAGAAAT   1380

CTGCATTTAT AGTGTCAACA TATAG   1405

          (2) INFORMATION FOR SEQ ID NO: 73:

               (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 1398 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

               (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CnTCAACTTC AGCTCTGTAG TACTATCTGC ACTAAAACTA AGCTTGACTC CACGCTTGTA   60

TGGATACCCT TTAGCAGGAT AATTTTCTAT TTwATCTTTA CTACTAGTAA AAACTCCATC   120

CGAATTGGAG TAAATTAGAT TTTTATCTCT AAAATCTACA GAATTACTAA GCAAACCAGC   180

ATCTTGCTGA GGATTTTTCA TTAATGCTTT AATTTCTGCA ACTTTTTTAT CAAAATCTTC   240

TTTTATTTTT GTAATACCAT CGCTCATTAA AAACTCCTTT AAGCAATACT TGTTCTTTTA   300

TGTCTTTTTA GATTCTCATA AAATTGAGCT CGTCTTTGCT TGTAAGTATT ACTTATCGCT   360

TGTACAAACT CCGTGAAATT AATGGGCACA AAATTAGAAT CAAGCAAACT TGCTCTCTCT   420

TCTGATTTAA CAACAATATT GCCTCTGACA GAGTCAACAG AAGAAGAATT GCTACTCCCA   480

GTTTTTCTTA ATTTAATATT CACTTTTGCT AAAGAAACAA GTTGTTCTAG TATCTCTCCA   540

TCGATATGAC TTATATCTGA CGCTTTAGCA ATAGCTTTAA TTTGCTCAAT TGGAACAAAC   600

TTACGAACAA GCTCTCTACG TTGTGCCTGC ATAATGTCTT TTAGGGTGTA TCCTTTTGCA   660

AGTAACACTT CCTTGTTAAA ATGGTTGCTA AGATGCGCTT TTACAAGTGT ATCAATTTCA   720

TTAATTCGCT CAGCCTCTAG TAACAATTGC TTTTCAACAC GCTCTCGATC TTCAACTTCT   780

GCAAGTTCTT TTGTTATTCG CTCATTTATA CTCATCACGC CTTACCTCTT TAGGGGGTTT   840

ACATTGTCTG TTTGCTCTTT AAAGCGCATG TACTCTTCAA ATTCCTGCGC ACTTATAACT   900

TTAGTATCAG CCTTATTTTG CTGCTCTTCT TTATCTTGTG CTTGCAGGTC TTCTTTTTCT   960

TTTTTCTCAG TCATCTTTTA ACTCCTTTTC TCAAAATGAG AATAATTTCT CTTTTAAAAT   1020

CGCTAGCTCC TCATTATCAA AGGmGCTACT TTGTATAAGC TGGTTATATT TACTGTAAAG   1080

CTCAATTAGC TTTATATCTC TTTCCACTTT TTGCTCTTCA CTTAACATAA TCAGAGAATT   1140

AAACTcATAT CAAGCCCGAA ATACTTgTAA GTTTCAAGTT ACAAGCGTTC TCAACTTGTT   1200

CTTGcACACC CTTTAAAAAA TCGTAATAAT TACTCCTATC CCCTTTACCA TCATTTCCTA   1260

GCCCTTTAGC CTGTTCGTTA AAACTTCTGG TTAAGGGCTC TTtAGTATCT GCACCAATTT   1320

TtGCCTtAAT TAATGCTAAA GCCTCCTTTA AGTAACTAAG GTCGTATTTA ATAACCTCTA   1380

AACTAGCACT AGGGGTGG   1398

(2) INFORMATION FOR SEQ ID NO: 74:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1380 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

ATAATAGGCC CAATAAAGAA TATTTTGAAC ATGAATAATT ATTTAATTAC CAATATAAAG   60

CTAAATACAA AATAAATTCA ATATATCTTT AAATTCTAGA AAATTTTTAA TCTAAAAAAA   120

TCATTATTAT AGTGCCCAAA ACAAAATAAA ACTTAAACTG GAAAATTAG TGTTACATAA   180

AATGAATAGG GCTTAAGACA AATTCTTTAT AAAAAACTTG CTTTAAGCCC TATTTCACGA   240

TCATATTGTG ATTCGAATCC GCGTCGAACT ATTTATAGTA TAACAAAAAT TAAATCATAG   300

TCAAGTTGTA TTTTAAATAA ATTTTAATCT TAATTACTAA AACTTTACAA TATAACTAAA   360

ATTGCTATAA GAGTATTTAC TTTTATAGCA ATTTTAGTTA TATTGTAAAG TGATCAATTG   420

TGAGGAGAAA CTTTTATGAA TTCAAAAACA ACAAATAAAA CCACTAGAAA TTGCTATAAT   480

AAAGTTCAAC ACAAATTAAT AGTTCTTATT TCAACAATAT GCTATCTAAA CAAAACACAT   540

AAGAAATATA CACAAAAAAC CATACTCTAT TATTTTAATA AAAATCTAAG AAAAAACGGT   600

CAACCTATTT CTACACTAAG AACTATGCAA AAGTATATTT ATAGACTACA AAAAGAAATA   660

AAAGTCACAA AAAACTACTA ACTATTTCTG ATAACAATAT CGATATCCAA ACCATGTAAT   720

AGAAATCCCA AACACATAGA GCCAGCCCCC CAAAATACAA GGAATTAAAA TCAAGCAACA   780

CATAAACCAT TTCAATAACT TCTAAGTATA AAATGCCAAA GCATAAATTT TGCTATTGCT   840

TAAACTATTT TCGAGTATAC ATCTGTATTA AATTTAAGCT TGTTTTTTCT ATCAATGAAA   900

TCATCTTTTG CATCCTTGTC AAATACAATT TCACTTTAAT TTTAATAAAA AATAAAATAT   960

TTGGACTCAC CAATAGGCTT CAGTGCCCGC ATTAAACCTA AATGTTTAAT TAAAAATTTT   1020

TGGATTGTTA TTCCCAATGC TTTTTCTATC TTGAAAGAAC TTTAAAAGTG CTTTCAAGAT   1080

AGTTTCTTTT TGCACGTTAC TTGAATTTAC ATTCAAATAA TAGGGCAAGT TGCTTTATAT   1140

ATACTCTTTA TTTTTTTTGA TTTTTGTATT TAAGTGTTGA TATTATTAGT AATATTTTAA   1200

ACTTTACTCT TAACTAAAAG CTTGTTTTAT TGTTAAAAAT AAAACACAAA CAATACCCTA   1260

TAAATAGTTT AATATTGCAA TATTATTTAA ACTATAAAAA TATGTAAATA ATAATTTATA   1320

AATTAATAAA AAACATATAA GGGAGCTTTC TTAATGAAAA TCAAAAATAT AGCAACATAT   1380

(2) INFORMATION FOR SEQ ID NO: 75:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1326 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TnAGAGCAnG GATCCAGGAG AAGTTAAAGA TCCTATAATG TATAAATGGT TTTCGCCTGA   60

TCAAATTGAA GATGTTGATC TTCAGATGGG CTACCAAAGA ACTGTAAAGT GGGATGCGTT   120

TTTAAATGCT AATCCTACAA CGATTGCTAA TGAGGTTAAT ACTATTTCAA CTATTGGATT   180

TAGTTCTGAA GTGGTAAGAC TTAATTACTT AAAATTACAG TACAAATTTA GGCACTTAAA   240

GCAGGCGTCT GAAAAATTTT ACACTTCAGA CTCATATCTT GGTGACATTA ATAACAATTT   300

ACTTCCTTTC TCTCAAGCCT ATAAGCTTGC AAGTAGCGAG ATTATTAAAC TTATTAATCA   360

CTTTGTACTA ACAGGCACTG TTTCAATTCA AAAAGATGGA AAAAATCAAA AACGTCTACT   420

TCCCAATATG TATGGACTTC TTAATATGCC ACATCAAGTA AAAGAAGAAG TTGCTAGTGG   480

TGATAAAGAT AAAATGGATA AAATATTTGA AAAAATTGAG GCGGGACTTT CAAAGTTAGA   540

1059

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GCTAGGAGAC GAATTTTCTA CACCTATGAT GGTAATAGTT GACCCTACAA CTTCGCTCAA      600

ACTCGTAAAG CCATACGCAG CAGCACAGGG TGCAGCAAGT AGCTGCGAAA AATGGGAGGA      660

TGTTTTGATT CAAACTATCA AGGCTATTAA TAATAGAGAA GATGTCTACA TTGAAACTTC      720

AAACTTGCTA AAACATCAAA TACTTATTTA CCCATTAAAC CCAGAGCTTA TTAAGTTTAA      780

ACCTAGCAaG TATATGTTAC CTACACCAAA TGaACAAGTG GATAAAGATT CAACTGATAT      840

TGcTCATTCA TACATTGATT TTGTTTTAGG AGGGTTACTT GCTACTAGAA AAACTATTTT      900

GCAAGTACAT ATCAAACAAA GTTAAAGTA  TAAGGTAAGT GAAAATGAGT GAACAAGAAA      960

ACTTACAAAC ACAAGTTGAG GCTGAAGAAG AACTTTTGGT AACAAAACTT TATTCTGAAG .    1020

TGTTATTGTT ACTAGGAATA GACAAACTTG CATTAAGCAG ACAAAATTTT CTACTTCATT      1080

TATCTTTACT TCAAGCTATT CTAGTAACAC GTGGTATTGA TGCTAGTTCA CTTACATATG      1140

AACAAATATT TTTACTTACC TTTTACCATA TGGGTTGTCA ATTAAGAAAA CAGGGAGTTG      1200

TTCGAGAATT TGAATTTGAT AGGATCAAAA AAGAGAAATT CAATGAACTT GAACTTGATT      1260

ATtATCCTAG TAGCAGTGGA GGCGAAGAAG GTGGCGAGGG GGGTTGTGGC TCAAACAAGA      1320

ATTTTT                                                                 1326
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(2) INFORMATION FOR SEQ ID NO: 76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1309 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

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GGGCTGCTAG ATTAATTGCA GGTAGCAGTT GCTTGATCTG CAAAATTATC TATATTGCCG      60

CCGCTAAAAA ACCCTTGAAC GGTAGTTTTG AAGGTGTTTT TTCCTTCATC ATTTCCATTA      120

CATTTATCAA GTTCAGTCTT TATATGTTCA AGTGCTGATT TAATTTTGCC TTCATCATTT      180

TCTAAGAATT TATCAAATTT TCCAACACCA GTTAAAGCGG TTTTTAACCA GTCAAGTTGT      240

GTTTTTTGAT CATCAGATAG CTTTTCTCTA AGCAGGTCTT CTTTAGATTT AGATTTAGGT      300

TTTTCTTGTG TTGCTTCTTT TTGGGTTAAA TCACGCTTTT GTCTGCTTTT TGTCTGCTTG      360

GTATTTGTAT CATTAGAATT ACAGCCGTTT AGCATTAGTA AAAACAAACA AAATAATATG      420

TTGATAATTT TCATTGTTAC TCCTTTTTTT ATTATTAATA TTCACTTAAC TAAGTATTAA      480

TACTAAATAT GGGATAAACA ATTATTATTT GAATTGATAT GTTTTAAGTG AGGTAGTAGC      540

TATTTAGAAA TGAAAGCAAA TATTAGCCCG GCTATCATTG TGATAGACAT TGCTCCCATG      600
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1060

ATTCCTAATA CCCATTTAAG CATTTCTGAA AGAGACATTA AATTCTTTTC AACATTGTCT   660

ATTTTAGTGT TTAAATTCTT TTCTACAGTA TCTATTTTGG CATTTAAATT CTTTTCCACA   720

TTGTCAATCT TAGTATTAAG TTCGCTTTTA ATAGCATCAA TCTTAACATG TAAATTCTTC   780

TCTACGGCAT CAATCTTGAT GTCTAAATTA GATATAyCCT TTTGTAAATt CTTTTCTACA   840

GTATCTATCT TAGTATCTAA ACTATCTATT TTTAGATTTA AATTCTTTTC CACATTGTCA   900

ATCTTAGTAT TAAGTTCGCT TTTGACACTA TCTATTTTAG AAATAAGATT ATCAAATTTT   960

ATATCaAATT GTTTTTCTAA ATTTTCTAAA TCTCTATATG TTAGCTCATT GTGATAATAT   1020

CTTTTAGATA AATCTTGTGC TATTAGTTGT TCCATGCCCA GCCTAATAAA TTCTTTATAT   1080

ATTTGTTCTT GAGTTACACT TGCAATATTT GTTGACACTG TTTCCATAAA ATTTTCCCTT   1140

ATGGTCATAT TATACACTAT TTTAGATTGA TTGGCTTTAG AGATTTTTAT ATGTAAAGGA   1200

GAATTCTTG CAAGAAAAAC CTTTTTGTAA TTTACATTTT TAACTGGGAA TATTTATTAT   1260

AGACTTTTTC CGCTATTGGT TTTGTTTTTT TAATGTACTC TAAATACTG   1309

(2) INFORMATION FOR SEQ ID NO: 77:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1300 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TATCTATATC ACCATTTTTA AAGAATTCTG TAACCACAGT TTTGAAAGTG GTTTTTTGTT   60

GTTCTGCTTG ATCACCATTA CAACTATCAA GTTGAGTTTT TATATGATCA AGTGCTGATT   120

TTATTTTATC ATCATCATTT TCTAAGAATT TGTCAAATTC TCCAGCACCA GTTAAAGCGG   180

GTTTTAACCA GTCAAGATGT GTTTTTTGAT CGTCAGATAG CTTTTCTCTA AGTAGTTCTT   240

CTTTAGATTT TGGTTTTTCT TGTGTTGTTT CTTTTTGGGT TAAATCACGC TTTCCCCGTC   300

TTTTTGTTTG TTGGGCATTG TTTTTTAAAG TGTCATTATC ATTAGAATTA CAGCCGTTTA   360

GCATTAGTAA AAATAAACAA AATAATATGT TGATGATTTT CATTGTTACT CCTTTTTTTA   420

TTATTAATAT TCACTTAACT AAGTATTAAT ACTAAATATT GGATAAACAA TTATtATTtG   480

AATTGATATT CTTTAAGTGA GGTAGTAGCT ATTTAGAAAw rAAAGCAAAT ATTAGCCCGG   540

CTATCATTGT GATAGACATT GCCCCCATAA TTCCCAATAC CCATTTAAGC ATTTCTGAAA   600

GAGACATTAA ATTCTTTTCA ACATTGTCTA TTTTGGCATT TAAATTCTTT TCTACAGTAT   660

1061

CTATTTTGGC ATTTAAATTC TTCTCTACAT TATCAATCTT AGTATCTAAA TTAGATATAT 720

CTTTTTGTAA ATTCTTCTCT ACATTATCAA TCTTAGTATC TAAATTAGAT ATATCTTTTT 780

GTAAATTCTT CTCTACATTA TCAATCTTAG TATCTAAATT AGATATATCT TTTTGTAAAT 840

TCTTTTCTAC ATTATCTATC TTGGTATTAA GTTCACTTTT AACAGCATCA ATCTTAACAT 900

TTAAATTCTT TTCTACAGTA TCTATTTTAG AAACAAGATT ATCAAATTTT ATATCAAATT 960

GTTTTTCTAA ATTTTCTAAA TCTCTATATG TTAGTTCATT GTGATAATAT CTTTTAgATA 1020

AATCTTGTGC TATTAATTGT TCCATGCCCA GTCTAATAAA TTCTTTATAT ATTTGTTCTT 1080

GAGTTACACT TGCAATATTT GTTGACACTG TTTCCATAAA ATTTTCCCTT ATGGTCATAT 1140

TATATACTAT TTTAGATTAA TTGGCTTtAG AGATTTTTAT ATGTAAAGTA rAATTTCTTG 1200

CAAGAAAAAc CTTTTTGTAA TTTACATTTT TAACTTCAGA TATCAGTTTT AAATTTTTTA 1260

CTGTAgATTT TTTACAAAAA CAGTATTGCA AAAACTCTnA 1300

(2) INFORMATION FOR SEQ ID NO: 78:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1295 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GAATTAATAA GCAGAGATGA TAATTTTTTA GGCGTTATTC ATGAACGTGA AGACTTGAAC 60

AAAAGGATAG CAGAAAACGA TACTTtCGAT TTAAATAAAG ATTaTATAAA AGAATATGaA 120

ATTACACTTG aAAAATTTTT TCAGTTGTCA AAAAAATTTT TAATTTCATA ATATATAGGG 180

AAATGAAATG AGTGTAAAAT TAAAACATAT GAATATAAAA ATAAAGATc GTATTAATAC 240

TGGcAAAAAT CAAAAGCAAA TTGaAATTAA TTGTGATGAA GaTAAAATGG AACGATTTCT 300

ATTTTTAAAA GAAAGGCTAA TAATCAACTT CCAAAAGAA ATTCACAATA AAATAGAAAC 360

AATGAAGATC TTAAAAGAGA TTAAAGATAA AGAATATTAT AAATTAGATG GCTATCAAAA 420

CTTTGAAATG TTTACTAGGA ATTACAAAAT AGCAAAAGC CAGGCTTATG AATATTTAAG 480

AATrGCAAAT GCAATAGAAG AAGGryTAGy TyrGGArAAA krCATAATCG AAAACGGTAT 540

AyAGAATTCT TTATTTTTTT TAAAGGATAA AGAAGGGGrG AAgTTAAAAA ATCCAATCGA 600

AATTTTATCA GGCCATTAAG ATTTCAGCTT AAAACAGAAG ATGCATACAT ATATTACAAA 660

TCAAAAkCAA GATTTACTAG TTTTTTGCTA GAAAAATTAC TTAAAGATAA AGAAGAATTG 720

CTTAATGAAA TTATGAAAGA ATATAAGGAG TGTAAAAAAT ATAATTAAAA ATTTAGTATA 780

```
GATAATTTTG TGTTAAGAAT ATTAACCTAT GTGATTTATC AAATATATTA TTTAGATAAG      840

GTATTTGATA AAAAACAGGG AATTTCTTTG TTTATAAAGT AGTTATTTAA ATCATAAAAT      900

GTCAAAAAAA TCGGGGTAGT AAAGTAAAAA GTAAAGATG  ATTTACAAAT AAATATGCAT      960

ATTATTTGAG AATAATGTAT TGATTTTAAC ACCAACAAAA TTCATTTTCC AAATGATATA     1020

AAAGTTTTTA TAAATGAGCT TATAGGGTCG TTTTCAAAAT TAGGCTATTA TAAAGAGGCA     1080

AAAGAAACTT TGCAAAATAT TTTTTGTATA TTAGATAGTA ATTAAAAATG ATTTAGTCTA     1140

CTCAATAATT TATATGAGAT AATAAAGTAT ATTAAGGATA TGTGCTTTAT TAATAAAAAT     1200

AAAAATAAAA ATAAAAATAA AAATAATTAT ATCTTAATAA AAAAATTGGA AATACCGCAA     1260

TTATTGATAA TTTATCGAAT TTAGATACTA ATATA                               1295
```

(2) INFORMATION FOR SEQ ID NO: 79:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1284 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```
TATCnTTTTT CCTCAAAAGT TTAATTGGAA AATAAAAAGT TATnCTCTGG TGATATTAAT       60

AATTTTATTA TTGGGAATTC ACAACGCTCA GTTGAAGTTA ATGTTTTGGG ACAATTTGAA      120

AAGCTATGTA AACTTCTTAA AATTCCTTAT ATCCCAAGAC ATACAAATAA yTCATATATA      180

TTAATTGATT CACTtCGTAT TAATCTATAT GGAGGAGATA AGGCAAGTGA TTTTGAAAGA      240

TTTAGAGGCA GTAATTCGGC ACTTATTTTT GTTAATGAGG CTACTACTTT ACACAAGCAA      300

ACTTTAGAGG AGGTCTTAAA AAGACTTAGG TGCGGACAAG AAACTATTAT TTTTGATACT      360

AATCCTGATC ATCCAGAACA CTATTTTAAA ACCGATTATA TTGATAATAT AGCGACATTT      420

AAGACATATA ATTTTACAAC TTATGATAAT GTGCTACTTA GTAAAGGATT TATCGAAACA      480

CAAGAAAAAC TCTATAAAGA TATACCATCA TATAAaGCAA GAGTTTTGCT AGGTGAGTGG      540

ATAGCAAGCA CCGATTCAAT TTTTACACAA ATAAATATTA CTAATGATTA TGTATTTACT      600

AGCCCGATAG CATATTTAGA CCCAGCATTT AGTGTTGGmG GGGATAACAC TGCATTATGT      660

GTTATGGAGC GrGTTGATGA TAAGTATTAT GCTTTTGTAT TTCAAGACCA ACGACCAGCC      720

AATGACCCGT ATATTATGAA TATGGTTAAG ACCGTTTTAG AAAATTTTAA TGTACATACA      780

yTTTATTTAG AAGATAGAGA CAATACAAAA GGTGCTGGTG GATTGACyCG yGAATACATs      840
```

TTGCTAAGAA ATAATATGGG TCAATATTTT AGAATTGTTC CAGTTAAGCC AAAGTCTAAT   900

AAATTTAGCA GAATAACArC GTTAATTACG CCGTTTAyTT ATAAGAAACT kTACATTACr   960

AAGTACAGCA GTTCTTCTGT ATTTAATGAT ATTTATTCGT ATAAAGGAGA TAACAAAACC   1020

CATGATGATG CTCTTGATGC AATATCTGCA GCATATTTGA TGTTGTCTTT AGGGTATAGA   1080

GAGAGAAGTG TTCACTTTGG CAATCAAAGA TTTTTGTAAA TTTTATTGAC AAAAATAATA   1140

GTTTTTGCTA TCATACATCT AATTTAATAA AGAGAAATAA AAGGTGTGTG ATTTAAGAAA   1200

AACAAAATTA ATAGATAAGA TAAGTTCACT AGAACTATAT AAATACTCAA TATTTTTTAG   1260

GAATTATATA GAAAATGTAG CAGA   1284

(2) INFORMATION FOR SEQ ID NO: 80:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1271 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GCTTGAAAAA TTTCTTTCGG GGCGCTTAAT GGAAGAATCA TTTCTTATTA GAATGTGGTT   60

AACTATTTTA AATTTTTTTC AGAAAGAATA AAAGCAAAGA AGAATATATA TAAAGCTTAT   120

GTTATAAAAA ACCTGGAAAA TCAAATTAAT GAAATGTTGT AAAAATCCAG TAATAGATTT   180

TAAGAAGAGA ATGTTTGCAT GTTGGTTTTG TGGAAATGTT TTTTAGTGTT TGCCGATATT   240

CAATGGAATT GAAAGAATTT TTTAGGAAAT TAGAAAAGG TGGTATTGTT GTTGAGCAAA   300

CTATTTTAGA AATTATTCAA AGCAAAGTTC TTAACTCTAA GAACAATTTG GAAGAATTTT   360

TTAGATGAAG GTGAATATGA GCTTTTTTTA AAAAAGAAA AAACCCAAAA CGAATTTAGA   420

AGAATCTCTT AAGGGTCAAG ATAAATGAAT ATATTAATTC TATTCCATCT AGTACTTACA   480

AAATCGTCTC GGATATGTTT GAGTTTTATT ATGTTTTTAA TAGTTTGGCG TTTTTCCCTT   540

ACAAATCTTT TTTTTCATTT TTTAATGTAG ACCTTTTAGA TAGTGCTGAG AATATTAGCA   600

TTGTTGACTT TGAAGGTTGG ATTTGGGGGG AATCCTCTAG AAGTCGACCT GCAGGCATGC   660

AAGCTTGGCA CTGGCCGTCG TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCC   720

AACTTAATCG CCTTGCAGCA CATCCCCCTT TCGCCAGCTG GCGTAATAGC GAAGAGGCCC   780

GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG CGAATGGCGC CTGATGCGGT   840

ATTTTCTCCT TACGCATCTG TGCGGTATTT CACACCGCAT ATGGTGCACT CTCAGTACAA   900

TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC GCTGACGCGC   960

CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC GTCTCCGGGA   1020

GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGAGACGA AAGGGCCTCG   1080

TGATACGCCT ATTTTTATAG GTTAATGTCA TGATAATAAT GGTTTCTTAG ACGTCAGGTG   1140

GCACTTTTCG GGGAAATGTG CGCGGAACCC CTATTTGTTT ATTTTTCTAA ATACATTCAA   1200

ATATGTATCC GCTCATGAGA CAATAACCCT GATAAATGCT TCAATAATAT TGAAAAAGGA   1260

AGAATATGAA T   1271

(2) INFORMATION FOR SEQ ID NO: 81:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1269 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GAATTTTTCA AAATTACAAA ACTTTAACCC AAAATGGTAA AACTTTAATT TTTTGTAATT   60

TTTACATAAA AGTGTTAACT TTAAAATyCC AAACTTTATA ATTTTGGAAA ATTATCAATA   120

CTTTTTTAAT TTATTCTTTA TTTTCAAAAT AATCTTTATA TACTTATATA TTATGTATAA   180

GTCTGTAAAA GAACAACAAG AAAAAGGAAT AGATCATACA TGCAGAATAC TTATTCTTAC   240

CGAAACAATA TTTGAAATAA ATTTAATATT AGAAAATTAT TCTCAAAAAA CTCTACTCAA   300

AAAGTATAAC GAAAATCTCA AAAACAAAAA TCTACCTCCT AGTAATATAT CAACAATGAA   360

AAAATACTTA AATCAATTAG AAAAAGAAAT AAAAATCATA GCAAAATTCT ATTTTAAAAA   420

CGATCAATCT CTAATTTATT ATAAACTTAA TTATACCCTA GAAAAAATTT GGTTAAAACT   480

AATAGAATTA TTCTACAAAG AATTAAAACA ATTTATACAA AAGAACACTA CTACTTAATT   540

GTAAATACAT TATAAAATAA TCTTATTCAA AACTTTAGAA ATATATTGTT TTACGCTAAA   600

AAAATTTAAA AAATACTGTG CCATATTTGT AATATAAATT TAATATAATA GGGGGCTAAT   660

TCATTATGGA TGGAGTAaTT AACGATACAT TGGTCGCAAG AATGAAAAAG CAAATTAAAT   720

TTAATAAGAA TAAGTTAATC ATTCTTGTCA AAACACTAGA TCATATGAAT AAAGAATTAC   780

TTTATAGTGC AAATAAAACT TACAATTATG TCTTAATACA AAACAATTTT AATGAGGCTC   840

TAGCTAAAAC TTATCAACTT AGGGTTAATT ATAAAACCCT ATTAGAATAT CTTGAAATAT   900

TAGAAAAAAA TCCAAAAGTA ATCTTAAAAC GTCCCACAAA TAAAGAAAAT GAAAGCTTTA   960

TAGGCCTTTA TACACTCCTT TACCCTTTAG AAGATTGTTG CACTAAAATT TATAATTCTC   1020

1065

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ATCCTAATAT TTAAGCTAAT ATAATCCAGA AAATTATTTT TGCGAAATAG CATAATGCTT          1080

TAGAGTATTA AAGGCCTAAT AAAGAACAAT TAAAACTAAA AAATATATAA ATAAACCGTA          1140

AATTAGGAAA ATTAATGTTA CACCAAATGA ATAGGGCTTA AAACAATTTC CTTTAAAGAA          1200

ATTTCTCTAA GCCCTACTTC ATTGCTTATT ATTACGTCAA TTCGAGCATA AAGCCGAACT          1260

AATTTATAG                                                                 1269
```

(2) INFORMATION FOR SEQ ID NO: 82:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1225 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```
CGGCCTTTTT TGTTGCAGCA TGATCAAGAA TCCCTTTAAA TTTAATGGTG AATTTGTCGC            60

TCACTAAGCC CTCACTTGCT TAAAATTAAT TCATACAATT CTTTTTCTAA TTTAATCTCA           120

GCAAGTCTAT TGACCTCTAA AgCTCGTCAT AAGGCAATTT CTTTACATTG TCGTACGAGC           180

AAaTATTCAT AATTACTGGA AAATAATATT TGTCGTTCTT AATCTCGTCA AGCAgTTAAA           240

ATATTTTTTT CTAGTCTCAT TAaGACTTGC AATAGCTTTA TCAATATCTC TATCTCTTTT           300

GCTCATTTAG CAACCAGCTC ATTGGAATTT GATGTACTTG ATGAAAGTGA AGTGGCTACT           360

TTTTCATAAT CAAAATTTTC ATTAATATAG TCAAAAGCAA CAAAATCACC AACATTATTT           420

TCATACTCAC TCAAATATAC TAAAGCGGGC TTTTTTAGAT CATTGTCTAA ATGAAAAGTA           480

TTAAATTGTG CAGTGTAAAT TATTGCAACA AGATAGTCCT TATAATAAGA AATAAATTCT           540

CTATTTTGAT CCAAAATCAC ATAGAATTCG TCTAAAAATT TTGGACTTAT CATTAAGCTT           600

GTGATTTCTC TTAAGTATTT AACCTCATTA AGCTTTAAAA CAGCGTCACT TTGATTAAAT           660

CCTAGCACCT TTATCCCATT CATAGACTGG TAATACTTTT AGTGGATATT CATAAGTTTT           720

ATTTTTAGTT AAAATTTTCA TTTTATATCT CATTATCATA ATAAGACTCT CCTTTTAAGT           780

GTTGTTTGGT TTAGTTTTTT GGCAATTAAT AGCCCTAATT TCAAAGATA CTTTTTCGGC           840

CTCAGCAGAA TAACTTCTTG AAGGCTCTTC AGTAAAAATT GCATAGTTAG AAATAATTTT           900

GGTAGCAATT CTATCATTGA ATACTAAATC AAGCATTTTA TCCTCTTTTC TCACATCCAT           960

GTTGTAAAAC TGTTCATCAG AAAGTTCAGT TAACAAAATG TAGTCATGAC TACCTAGTGT          1020

CACTTCAATG TTGAAAACAT AAGTTATTGT TTTGGGATCT CTTAAGCTTA TTACAGGCAT          1080

ACCTTTATCT TCACTACTAA TCACTGCTCT TGTTGTAGGT TCGCTTGTAA GCTCTAGCTT          1140
```

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GCCACTATGT AACTGCGGTA CCACCAATTG AAAAATAAAC TTCTCTTAAA TCATAAAATT      1200

GCATTTTTAG ACCCCCTTTT TAGCA                                           1225
```

(2) INFORMATION FOR SEQ ID NO: 83:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1200 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```
CGGCTGGTGC TGTTAGTGCT GTTAGTGGGG AGCAGATATT AAGTGCGATT GTTAAGGCTG        60

CTGGTGCGGC TGCTGGTGAT CAGGAGGGmA AGAAGCCTGG GGATGCTAAA AATCCGATTG       120

CTGCTGCTAT TGGGAAGGGT GATGCGGAGA ATGGTGCGGA GTTTAATCAT GATGGGATGA       180

AGAAGGATGA TCAGATTGCT GCTGCTATTG CTTTGAGGGG GATGGCTAAG GATGGAAAGT       240

TTGCTGTGAA GAGTGGTGGT GGTGAGAAAG GGAAGGCTGA GGGGGCTATT AAGGGAGCTG       300

CTGAGTTGTT GGATAAGCTG GTAAAAGCTG TAAAGACAGC TGAGGGGGCT TCAAGTGGTA       360

CTGATGCAAT TGGAGAAGTT GTGGCTAATG CTGGTGCTGC AAAGGTTGCT GATAAGGCGA       420

GTGTGACGGG GATTGCTAAG GGGATAAAGG AGATTGTTGA AGCTGCTGGG GGGAGTGAAA       480

AGCTGAAAGT TGCTGCTGCT ACAGGGGAGA GTAATAAAGG GGCAGGGAAG TTGTTTGGGA       540

AGGCTGGTGC TGGTGCTAAT GCTGGGGACA GTGAGGCTGC TAGCAAGGCG GCTGGTGCTG       600

TTAGTGCTGT TAGTGGGGAG CAGATATTAA GTGCGATTGT TAAGGCTGCT GATGCGGCTG       660

ATCAGGAGGG AAAGAAGCCT GGGGATGCTA CAAATCCGAT TGCTGCTGCT ATTGGGAAGG       720

GTAATGAGGA GAATGGTGCG GAGTTTAAGG ATGAGATGAA GAAGGATGAT CAGATTGCTG       780

CTGCTATTGC TTTGAGGGGG ATGGCTAAGG ATGGAAAGTT TGCTGTGAAG GATGGTGGTG       840

AGAAAGGGAA GGCTGAGGGG GCTATTAAGG GAGCTGCTGA GTTGTTGGAT AAGCTGGTAA       900

AAGCTGTAAA GACAGCTGAG GGGGCTTCAA GTGGTACTGA TGCAATTGGA GAAGTTGTGG       960

ATAATGCTGC GAAGGCTGCT GATAAGGCGA GTGTGACGGG GATTGCTAAG GGGATAAAGG      1020

AGATTGTTGA AGCTGCTGGG GGGAGTGAAA AGCTGAAAGT TGCTGCTGCT ACAGGGGAGA      1080

ATAATAAAGA GGCAGGGAAG TTGTTTGGGA AGGCTGGTGC TGATGCTAAT GGGGACAGTG      1140

AGGCTGCTAG CAAGGCGGCT GGTGCTGTTA GTGCTGTTAG TGGGGAGCAG ATATTAAGTG      1200
```

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1182 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```
GCTACAGAAA TAAAATTTTT AACAACAATT ATTTTTATTA TTTCGGCCTT TTTTCTCAAA        60

TTTTTATTGT CCCAAAAAGG TAACAATAAA ACGAATAACC TAGAAGAGGT GGCCAATTTG       120

TTATTTAAAA ACTTTAAAAT TTTTTGCAAT GCATTTTAAA TTCCAAATTA CTTTTGCATA       180

AATAAATAAA CTTCTCTTTG CGCAAATGGA AATCCAAACC GATCACTAAA ATATTTCTTA       240

AAAAATTATA TTCAGCTAGC CCAGATATCA TTTGCTTTTC ACACTGAAAA GCATCCTCTT       300

GAACACTAGA ATTAAAAACA CACTGTTTTT AAAATTTTCA ATTTAAATTA AAGATTGTAT       360

TTTGGCAAAA AATTTTCTAT ATCTATTTTA TATTCTCTGT CTTCATTAGA AATTAACATA       420

ATCTTTAATC GTTTTAATTT TTTGATTTTC TTAAAAAACC CTTTAGAAAT AGTAACACAC       480

AAGGTATTTT TTACTACAAA AGGAAATTCT AAATGAAAAA ACTTTTCATT TATATTCGGA       540

TCACCAATGT TAAAATCTTT TAATTGCTGC CATTTCTCAC TTGGTAAATT ATTTTCATGC       600

TTTGAAACTT TAGCATCTTC AAATCCTTCA AAAATTACAC TTTTAAAACC TAAAATTTTA       660

TTGTCATGCA CTTTAAAATC AAACCTATAA ACGGTAGATA ACGCTTTATA AGCATCTGCA       720

CGATAACCTG TCGCTTTTAT CATCTTTTTA TGCTTAAGCT CAGGAATTAT AAGCTGTGAT       780

TTTATAAAAA CCAATTCTTT CAAATTACTA TCTTTAAAAA GATATGTATA GGTTTCATCA       840

ACAAAAACAT TATCATCAAA CTTTTCAACA ATTTTATTAT AAATAACATT GTTTTCTTTT       900

TGTTTGTAAA AAAAGAAACC TAAAAAAATA CAAATTAATA GTAACCCAAA AAATAATATT       960

TTACCCATTA ATAATCTATC CTACTTATGA AAAATCATAT CAAATGCACT ATAAAAATGT      1020

GAGCTATTTT CCCTGCTTAC CCTGAAAGAA TATTTTTTTT CTCATTATTT ATCTCATCAA      1080

AACATTCAAC ATATACATCA ATTCCATTTT CTTCTGGCGA ACTTTCTTAT TTTATTCCAT      1140

TTTTTCACTG GAAATCCAAG GAAACTCATA TCCAAAATTT AA                        1182
```

(2) INFORMATION FOR SEQ ID NO: 85:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GnACnAGGAA CCGGCACTGA CGAGTCATTT AGACTGATTT TCAAGACCTT TTTAAATGTA   60

GACATTGAAG TTACTACTCC TGAAGCTGGG GTTATTGATA TCTCTTTAAA AGGGGTAATA   120

AAAACAAACT TTACTACATT TATTTCGCCT AGCACTAAGA AAGGAAAACG ACTAAAAAAG   180

ATAATTCTTA GAGAAAAGAA GCCGGGATAC GCTGCATCTA AAAAGCTTT AGTATTTAAC   240

TCACTTCCTA AaGGCTAtGA TCATTCAATT TATGCTTTTA TTAAGAGAAT TATTCCTATT   300

GGTAGAGTTC TCAAAATTAA TAATACAGAT GGTAACAATA TTATTACTTT CAATAACTAA   360

GGAGGTTTTA TGGCTGATGA TCAAGAAAAA TTACTGATTG ATGAAGAAGA AACGGTTCAA   420

ATTAAAGATT TAAATAAGGT TACGACCGTT AACAATACTG ATCTTTTACT GCTTGATGAT   480

GGAGCTGCAA GCAGCAATGC TATCACCTTT AAAAACTTCT TAAAAACCGT TAATCACCAA   540

ACATTTAAAG GCGAAGAGCT AGGCTATTTT AAAGAGATAA TTAAATCTAC AATCGCTACT   600

GAACTTGCAG CTGATAAAGA TTTTATAAAA AGCATTTACG ATTTAATCGT TGACAAGCTA   660

ATTGAGAATG AATCTAGTAA ACTTTCAAAT CTTTTTAGTA AAATCAAATC GCGCCTTACA   720

GATAGCATAT CATCAGCCAC TTTATCTAGA AGTGATGATC TTTTGATAAT GCCTTCATCA   780

GATACTATTC AAAAAACACC CGTTCCTAAA CATATACTTG GAGTACCATC AAATTTTACT   840

TATGGCAGCA TAACTAGAAG TACTACACTT TATCCTTCTG ACTATGAGAA TAAAGCGATA   900

TCTATTAATA TGGAAGACAA TGATGATGTA ACTCTTATTT TTTACAAAAA TTACGATAAT   960

GATCCCATTT ATCTGGATAT TGAGATTCAA GTAAAAATCA ATGGATAATA GGATGCAGAA   1020

AAAATCATTA AAACTTATGT nTTCTGATGA AATTACATAC AATTGGGTTT ATGAAATACG   1080

GGCCCTCGCG GACTATTCAC CAGAACTCCC ATTATAACGG AnGGTATATC CAAAAAGAG   1140

CCTCCTGTAT GGAGATCGTC CCGATCTTTA AAACTGTA   1178

(2) INFORMATION FOR SEQ ID NO: 86:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1177 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CATATGTATA ACAAAAATTA TTTTTGTCAG GCTTTTTACA GAAATTATTA TAATAAATAA   60

AAGCTTTATT AAATTCTCAT GTTAAAGAGC TTAAGAAAGC CGCTGGCTTA GCTCAATTTA   120

1069

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TTTTAGATAA ACTCACTAAA CAATTAAATT CAGTTCAATT TAGAATTAAA ATTATTTTGT       180

ATTTGTTAAA ATAAAAGAAC CTATTTAAAT TCTCTTGTTA AAAAATTCAA ATAAGTTCTA       240

CTTTAAAGCT ATATACTAAC TTATTACTTT ATAAAATTTT AATCATTCTT AATTTAAAAA       300

ATGCTTATTG AATATAGAAT AAATAATTGG AGCAAGCGTT ATTCCCATTA TTAAAATTAC       360

TTGTATTGTT CTATTACTTG CAGTAAGTTC GTTTTTTAAA ACATTTATTT TATTATCTAG       420

GCTAAATATA TCCyTTtGTA AGGTTTTTTC TACACTATCT ATTTTAGtAT TCAAGCTaGA       480

TATATCTTTT TGCAAAGTTT TTTCTACATT ATCTATCTTA GTATCTAAAC TATCTATTTT       540

AGAATTTAAA TTCTTCTCTA CACCATCTAT TTTGGCATTT AAATTCTTCT CTACAGTATC       600

AATCTTAACG TCTAAATTGG ATATATCTTT TTGTAAATTC TTTTCTACGC TATCAATCTT       660

AAAAATAAGA TTATCAAATT TTATATCAAA TTGTTTTTCT AAATTTTCTA AATCTCTATA       720

TGTTAGCTCA TTGTGATAAT ATCTTTTAGA TAAATCTTGT GCTATTAGTT GTTCCATACC       780

CAGTCTAATA AATTCTTTAT ATATTTGTTC TTGAGTTACA CTTGCAATAT TTGTTGACAC       840

TGTTTCCATA AAATTTTCCC TTATGGTCAT ATTATATACT ATTTTAGATT AATTGGCTTT       900

AGAGATTTTT ATATGTAAAA TAGAATTTCT TGCAAGAAAA ACCTTTTTGT AATTTACATT       960

TTTAACTGGG AATATTTATT ATAGACTTTT TCCGCTATtG GTTTTGTTTT TTTAATGTAC      1020

TCTAAATATA TGTTAATATT ATGTCTTACC GCAGTTATGG AGTGnCGTC TTTTAGnGTT       1080

GATAAGTCTG GATAAGGATA TCnGGATAAT TGGATCATTA ACTTTAACTT TTGGTTTAGC      1140

CAAAAAnGnT ACCAGGnACA TAACATACTC TGAAAGT                              1177
```

(2) INFORMATION FOR SEQ ID NO: 87:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1137 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
TCACGnCCAT GTtGtAAAAC TGTTCATCAG AAAGTTCAGT TAACAAAATG TAGTCATGAC        60

TACCTAATGT CACTTCAATG TTAAAAACAt AAgTTATCGT TTTGGGATCT CTTAAGCTTA       120

TTACAGGCAT ACCTTTATCT TCACTACTAA TTACTGCTCT TGTTGTAGGT TCGCTTGTAA       180

GCTCTAGTTT GCCACTATGT AGCTGTGTAC CACCAATTGA AAAATAAACT TCTCTTAAAT       240

CATAAAATTG CATTTTAGCC CCCCTTTTAA GCACTTAAGC TGTTTTGATA ATCAACTATA       300

TCTTGAGTAG TGATTACTAA AGCAACAGCA TTAATGCTAA AGTTATAAGT AATATTCACA       360
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1070

CTAAGTTCTA ATTTAAGTTG TGGTGTAGGA GAAAGGGTAA GGTTTAAGTT TTTATACTCT   420

ATAATCAATC CCCTGTCGAC AAACCTTTTA AGAAGACATT CAATTGCTGA AGTATATGCA   480

TTGTCTCTAG CACCACTAAG TTGTAGTGCA GATAATTTGC TATTTTGCCT ATTGTTTTTG   540

TTCCAAATTC TAATAAGCTC AATAATCGCT TCATTTTTA TATAATGATA AGTGAAAAGC   600

TCGTCTATTG AACTTCCAGC AAGATCAACG CTCTCTTTAA AGGCAGGCAT ACCATCAAGA   660

CCAGTTTCAT TAAGAAGTGA ATAAAGTTG ATTTTTGCAG TTCGCAACTT TCCAATTACA   720

GTATCATCAA CAAGTGGTGT AGCAGCCAGC GGCATGCCAT AAGGATTTAC AGCATGAAAA   780

ATACTAGCCT GATGTAAATA TTGACTTATA AATTTGAGGT GTAAATTGTC TTTATTATTA   840

CTGTAAACAG CAATATTTCT TTCTTTTTCA GTATTGCCTT TATCTTTAAA TAGTTCTTTT   900

ATTTCTTGTT CTTTAGTCGA GAATACAAAA AAAATTGAAG GTGTTTTAAA CTTATCATAA   960

TCATCTTTAT AAATCTTAAG TCCATCATCG GAATTATCAC CCTCAGTATT AATAAGTACA   1020

ACAAAAGTGT GTCTATGTAC TTTAAGATAT TTTTTTAACT CTTCGGGTTT ATCCTTATAA   1080

ATAAAAAGAA CAGCGGATTT TAATGATTCT TCACTTGAAT TGAAAAAATT TGACATT   1137

(2) INFORMATION FOR SEQ ID NO: 88:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1091 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GTGATTTTTG AAAGATATGG ATGATTGTAG GTATTTATGA TGTCGCACTC AAAATTATTT   60

TCAGGTGCAT ACGCCTTAAA CCCTTTAAAT ATTTGAGTTA AATGATTTAA TACCATATCT   120

AAAGTGAAAA TCATTCAAGT GTTACCTTAT AAGTAATCTC TGATAACATT TTGGCTGTAT   180

CAACAAGTGG AATTGCTGCA GTGTTACTAC CCCTTTTAAA CTTACTTTTG ATTGTATTAG   240

CCTTTAAGGC TGGAGTGACT TGTGCTGATA GTAGATAATT TTCATAGTAC CTTATAAAAG   300

CTTGTCCAAT AGCCTCCATT CCCTATTTAG GGTCAAGATT AAACTTAGAA TTTATATAGC   360

TATTATTGAT ATATTCTCTA AACTCArAAC TACTAGcAAT TTTGGTTAAA TGTTTTCTTG   420

CTGGTAAATT GCTATTCCCT TTTTCATGCA TTTTAGCAAT ACCTGCACGA CCACCAAACC   480

ACCCAATTTC CAATTCCATT TTAAATTCTA GTTTGTCCAT ATAAATTCCT TTAAAACCAA   540

AGTAAAATAT CCGATTGAAG AGTCAATACT AAATATTTCA AAGTAAACTA AATCTGCAAT   600

TGATATTCGG TCTTTTAGTT CATAGTTAAG GTCTTGATAT GTGTAAAGTT TGGAATATCC   660

TTGAATATCA GACATATCAG AATCATAAAG AATTGCAAGT TCTTGTGGCT TTATGTCAAT   720

AATAACTCCT GCGAATTCAG TGTACTTATT TTTATCAAAT ACTCTCTGAT AAGAAGAATC   780

ATTTTCAAGC TTTACAACAG TACCTTTATA AAACTTTAAG GGTTTAGGAT CCTTAAATAC   840

GTTGATCATr CGAAATGACA TATCAGAAAG TCTTTTyCTA ACACCATTCA TTAGACAACy   900

CCCACACAAG ATGGCGTTGA AGTTTCTCTT TTTArTTTTT CTAAAAATGC ATCAAGTTGT   960

GAACAAAAAy TCTTGTTTGA GCCACAACCC CCCTCGCCAC CTTCTTCGCC TCCACTGCTA   1020

CTAGGATAAT AATCAAGTTC AAGTTCATTG AATTTCTCTT TTTTGATCCT ATCAAATTCA   1080

AATTCTCGAA C   1091

(2) INFORMATION FOR SEQ ID NO: 89:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1081 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GGGAAATAAA TTCAAGAAGC AGGTATAATA ATTTTTATAA AAAAGAAGCA GATTTTTTAG   60

GTGCTGCTGT AGAACTTGAG GGGGCTTATA AAGCTATTAA GCAAACTTTA TTATAGATCA   120

CAAGGTATAA ATTTAAGGCT TAAGCCAATT TATCAAAAGA GAGGCATGTT TCTTGGTTTA   180

AAAGCATACT TTGCATACTT CTCTTTTGAG TACTACTATT TGAAAAGCTA TAAACTTTAA   240

CCTAATAGAA AAGCCAAATC TTTTTAAAAA TTTCTAAAAA ATAATTCTAC ATACTCTCCT   300

TATTACATTA AAAAATATTA TTGCTTATAT AAGGCACATA GTATAAAGAC ATTAATCAAA   360

ATTACCTTTT ACTAAGGTTT CAATCTCTCT AAACATGGAT AAGAACTACT TGATCAAGTT   420

ATAACAATCA AAACCCACTT TCTTTAAATA AAAAATCTTT TAATAATAAA ACCAAAATTC   480

CAGCCTTACT AAAGACCCTT ACTCTCTCGT GGATTTAATC TTCTTTATAT ATAAGGGTTA   540

GGCGTATCTA AAGATTTAAT CATTTTGAAT GATAGGGAAG AAGAATTCAT AAAGAATAGG   600

CAAAAGTGGT TTAGTTTACT GGAGCATATA CATTTAATTA TAAATAAGAA ACAATATTTT   660

CCATAAGAAC TGGAGTATAT AAATCATAAG AATAACTATT TTATAAAGAA TAAGTAAAAG   720

TAGTTTAGTT TACTGGAGTA TTTATCTATG TTAAAAGTAA ACGCACGGCG TATAAAGCCC   780

CTACTATAGT ATCCAATATT TTTTGAATTT AGGTCAATGT TGTTTAGTGT GTAAATAAGA   840

ATTATTAAGT GTGAAGATAG CCTATTTTTG CTATTCATAC TTAATATTTC TTTTAAAAAT   900

```
TTTTCCAAAT AGTGCCCCAG TAATTTTTAT TATTTATCAA ATAAAAATAT ATGTCTTTAC    960

ATTTATATTT CTAAATTGCT TAATTTGCAA AGAAATATTT TTTACGATTA AATAGTAGTA   1020

GGATAGTTTA GTTCTAACCG GAGTTTTAGT TTATCTGGTA TTGGTTGATA GTAGnCnTGT   1080

A                                                                   1081
```

(2) INFORMATION FOR SEQ ID NO: 90:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1078 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```
GATCCATATG TGTCCCCTTT ATTTTTAAAT AAAAGATATA TATTTAAAGA CAGTTAGGCC    60

TCTTTTAGGC ATATTTTTGT TTAATAAAAA ATATTAAATT AGGGTTTATA ATTTTTATAG   120

ATGAAAATAA AATAGAAGAA TCTAATTTAA CTAAACAATT TTTGTTTAGT TAAAATGATA   180

TAGGGCTTTG CAAAGTAGAT ATAATTAAAG AAAATCTAAA ATCGCTAAAT AAAACTATTT   240

AAACTAAGCC CCATAATGAA AAAGTTTTAG TAAAAATATT AAAGAATATT TTTACTAAAA   300

TAAAAATTAA ACCAGCATTA ATAATACTTA CATTAGATGA TTAGCTACTT TTTTTAATTA   360

ATAAATTTTG CATTTAAAGT TCTATTCCAC TTATAAATAT TGACTATATC AATAATTTTT   420

CaAGCATTGG TACATTTTAT ATTCtAAATA TTTCGTTTTG TCGCTAATTT GTTGACATAG   480

GAATTATAAA AAGGCCATCA TCTTTTAAAT TAAAAGTAA AATAATACTA ATAAATAAAG   540

ACCATCAAGC CCCGTCTTTT TTTTACTAAT AATACAATTG CATTGATTAT GGTTGTTATT   600

GATATTATTT TTTACTTTGA CAATGAATAT GAAAAAATTC TTTATTCTAA ATAAAGAAAT   660

TGGTATTGGT AATTGCAATT TATTATTTTA TTTATATTTT TTAAAAAATA TAAATAAAAT   720

ATAATAAAGA TTTATGGTAG AAAGCAAACA TCAAAAATAT TATTTTTATT CATTATTTTT   780

GTCAGAACTT GCAAGGACTT TGCCACATGC TGTATTAACT ATTATTTTAA TAAATAAAGG   840

GTTATCACTA AAAGATATTG CTATGGTACA AATTTGTTAT ATGGTAGCAA TTATTATTTT   900

TGAATTTCCA TCAGGTGTAA TATCAGATAT TTTTGATAGA AAAATTGTTT ACTTGGTGTC    960

AATTTTTCTA TTAaTGmCTT CTTATTTTAT TGTTGCTAAA ACCTCTTCAT TCGnGTTTAT   1020

TTGTGTTTCA GGTTTATAnA nGGGATGTCA GCnGCnATAG CACTGGCACG ATGACATA    1078
```

(2) INFORMATION FOR SEQ ID NO: 91:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1030 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CCATTTTAAA AAATCAAATT TTACAATACA TTATTATTTG CCACCTTGTA AATATTTCAT   60

AAATAGGGCA TTCAAAATTG GCCCTAGAAT TGCTGCTGTT ATTATCATAA AATGTACTAG   120

TCTGTTACCC ATGCTAAGTT TTTGATTTAA ACTCTTTTCT ACATTGTCTA TTTTGATATT   180

CAAGCCATCC ATTTTTAGGT TTAAATTCTT TTCAACATTG TCTATTTTAG TGTTTAAATT   240

CTTTTCTACA GTATCTATTT TAGAGTCTAA ATTATCCATT TTTAGGTTTA AATTCTTTTC   300

AACATTGTCT ATTTTAGTGT TTAAATTCTT TTCTACAGTA TCTATTTTAG AGTCTAAATT   360

ATCTATTTTT AGATTTAAAT TCTTTTCAAC ATTGTCTATT TTAGTGTTTA AATTCTTyTC   420

TACAGTATCA ATCTTArTrT CTAAATTAGA TATATCCTTT TGTAAATTCT TTTCTACAGT   480

ATCTATCTTA GTATCTAAAC TATCTATTTT TAGATTTAAA TTCTTTTCCA CACTATCTAT   540

TTTGGCATTT AAATTCTTCT CTACACCATC TATTTTGGCA TTTAAATTCT TCTCTACACC   600

ATCTATTTTG GCATTTAAAT TCTTCTCTAC AGTATCAATC TTAACGTCTA AATTGGATAT   660

ATCTTTTTGT AAATtCTTTt CTACGCTATC AATCTTAAAA ATAAGATTAT CAAATTTTAT   720

ATCAAATTGT TTTTCTAAAT TTTCTAAATC TCTATATGTT AGCTCATTGT GATAATATCT   780

TTTAGATAAA TCTTGTGCTA TTAGTTGTTC CATACCCAGT CTAATAAATT CTTTATATAT   840

TTGTTCTTGA GTTACACTTG CAATATTTGT TGACACTGTT TCCATAAAAT TTTCCCTTAT   900

GGTCATATTA TATACTATTT TAGATTAATT GGCTTtAGAG ATTTTTATAT GTAAAATAGA   960

aTTTCTTGCA AGAAAAACCT TTTTGTAATT TACATTTTTA ACTGGGAATA TTTATTATAG   1020

ACTTTTTTCG   1030

    (2) INFORMATION FOR SEQ ID NO: 92:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1028 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

TTTTGTTGAA TTTCCTGTTA AATTTTCTGA ATTGGTGTGA TTGCTTGTGT TTTTTAGATT   60

TCTAGAATTG TTGCTTCGTT TTGTTTTTTT TAGACTTTTA GAAGTGGTAG GATTTTTTGG   120

TTCGTTTGGG TTAACATTGC CAAAAGGTGC ACATGATATG CAAATTGAAG TTAATATTGC   180

TGTAATAACG TTAAGTTTAA TAATATTTAA TTTAAAGTTT TTCAAAATAT TCTCCTTATA   240

AATTTGAATT AATATTTATT AATTTTAGTT CAAATATATA ATATTACAAT TTAATATCAA   300

TATCAAATAA GTTTAATATT ATTTGATATT GAAAATTTAA TTTCTATTGA TGTTTTTAGC   360

GTGGATTTAG ATTGCATGAA TTTTAAAAAT AAAAGTTAAT TCTTCTCTTT TTAAAATATG   420

AAGTGTAACA ATTTGTTTGG ATTTAATGGG TTTAATCTAA GGATCAAGAT GAGGAATTTA   480

GAAATTATAA CGAACTAAAA GAACAATTAA AATTAAATTT GAAATCTGAT ATTAATAATA   540

AAATTCAAGA AATGAAAATT CTACACGAAA TTAAGCAAAA ATAACTTTAT AAATATGACT   600

GTTTTAAAAG TTTTAAGCAG TTTATAAAGT CTTATGTAAT TGCCAGAAGT CAAGTGTATA   660

TGTATTTGAA AATTTATGAG AAAGTTTTAG AAGGGTTTAT TTCTATTGAA AAAGTTAAGG   720

AAATGGGGTT TGTAGCTGCA TATAAAAATA TACTAAAGAA CAACTCGTCA TATGTATATA   780

AAGAAACAT GATTGAAGAA AATATAGCAG AAGATGGTGA TAGTCAAAAT ATGTCTATTA   840

AAATTTTAAT TAAAGATAAA GAAGTTTATG ATTTTTGCAA AAAAGATACT AAAAGAATAT   900

CTTTTATTTT AGGGGGGTTC ATTAAAGCAT TATTGAATTA AGTTGGAGAA TTTTTCTTTT   960

TGTATTTTTA TTAGCAATAT ATTTTCCCAT AGAGGCTTTT TGTGTCTACT AGAATAGGTA   1020

ATAAGATT   1028

(2) INFORMATION FOR SEQ ID NO: 93:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1002 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

AATTTTTnAA AAAAAAAAT TTTTTTTTA AACCCCCAGG GnAAAATTTG GGGAAAACCC   60

CCCCAAGGCC GTCCTTTATG GGTCCTGCCT TTAGCCCCAG AGGACGTTAA AATTGGATTT   120

ATTCAAACTT TTTATAATTA AAAATTGGCAC TGTAAGGAGT TTAAACAACA AACTCAGAGG   180

CTATTGTTAC AATACCCGAA TTTGAAGATT TAGAAATTCA CACAAAAAAT ATCTCTAATA   240

TCAGTTTAGA ATTATCAAAA GGTGATAACG TATTGCTACT TCAATCAAGC GTTAATATTT   300

TTGATAAAAA TAACGATAyC CACTTTGACA AACATCATTT TTATATACTT AGTGCAATTA   360

1075

GCCCAAAGAC TTTAAATCTA ATTTCTGATA CTGTTAAAAT TAAAGCAAAC AATAAAATTG 420

AAATAGCCAA TGAAATAACT TCCTTAAAAT CAATTCTAGA GAGTATTGTA AGTGCTATTA 480

ATGGAATTAC TGTAAAAGGA CAAGCGGTCG TTGACTATGC AAGCTTACAA ATAGCAACAT 540

CTAGAATTAG CAATAATATT AATAGTTTGT TTAAGTAATT TTTGCTAATT ATGGTATAAT 600

TACTAGTATG GATTTAAGAT TAGGCAATAA TTTTGAATTG GTATTTAATA AAGATATATC 660

ACTTGTTGAT GGAATTGATG AACAAAAACA AAGaTTTTTG ATATTTTTAA AAACCTTAAG 720

GGGTAGTTTA AGCTATGCTC CTCATTGGGG ATTGGACTAT TTCTTACTTT TAAAACTGTT 780

AAAAATTAAC AATCTTCACG CTGTAAAAAA TTATTTTCAT GAAATATCTA AAGAGCTTAA 840

CTTAGrTTTA ATAAATATTT CAACTACTAT ACAAGACAAC AAAGCACATA TATCCyTTTT 900

TTTCTCGGGC GATGTTTTAA ATATGGAGtT TAATTTaTGA GCtAGTTTTT GATTCTGrTT 960

TgGcwTTTAA AACGTACAtT AAGGgTATTG TAAGAGCTAA AA 1002

(2) INFORMATION FOR SEQ ID NO: 94:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 998 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGGCATTATG TACTGATAAT GATGATGCTT TAGAAGATCT TTTTAAAAAG AATGCTGAGC 60

TTAAGAGTAT AGAATATTGG GTAAATATTT TAAAAAAATA TTTCAATAAA ACTAATAGAT 120

TTGATGATCT AAATAAGCTT AAAGTATTTA TGTCTGATAA TCGAGACGTT TATAAAACAA 180

AAGTATTAAA ATTCTTTTGC ATGTTGAAAA AAGAAGACA ATTTAATTAT ATATTTGCAG 240

CATAGCAATA TTAAAGCCCC CAAATAGGGG GCTGTTAGCT ATTAGGAACC ACCATTGTTG 300

CAGTTACTAA CCGCATTGTT TGCAAAATTA TCTATATTGC CGCCGCTAAA GAAACCCTGA 360

ACTGTTTGTT TGAAGGTGCT TTTTTGTTGT TCAGAATTAT CCCCAGTACA CTTATCAAGT 420

TCACTCTTTA TATGATTAAG TGCAGATTTT ATTTTGCTTT CATCATATCC TAAAAATTTA 480

TCAAATTCTC CATCATTACC CAGAGCTTCT TTTAACCAGT CAAGGTGTGT TTTCTGGTCT 540

TCAGATAGCT TTTCTCTAAG TAGTTCTTCT TTAGATTTAG GTTTTTCTGG TGTTGCTTCT 600

TTTTGGGTTA AATCACGCTT TCCCCTGCTT TTTGTTTGTT GTGCATTGTT TTTTAAAGTG 660

TCATTATCAT TAGAATTGCA GCTATTTAGT AGTAGTAAAA ATAAACAAAA TAATATGTTG 720

ATGATTTTCA TTGTTATTTC CTTTCCTTAT CTCCAGTACA ATATGTTGAG TAAAAATAAA 780

ATTTATTCTT GTAATTATAG AGCTTATTTT TAAAAATCTT TAAAAATATT AATTGAGAGA   840

TTTATATTTT TCGAATGTTG TGCTAGCnTT TATTTCATTA TTATTGAATA TAGGAGTAAC   900

TAATGAGAAA TAAAAACATA TTTAAATTAT TTTTGCATCA AGGGATTTGT AATGGCTGTA   960

AAGCATATGT AGAAGAAAAG AAAGAAATGA TCATAATG   998

(2) INFORMATION FOR SEQ ID NO: 95:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 996 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAAAATATTT TTATTTATAT TTTATTGTAA TTATTCTTAA ATGATATATA ATATCAATTA   60

AGAATAATTA TTATTTATAA TATATATTCC TACTTAGATA AAAGGAGATA TTTTTATGAG   120

AAAAAGTTTG TTTTTATATA CATTATTAAT GGGAGGATTG ATGTCTTGCA ATTTAGATTC   180

CAAATTATCT AGTAACAAAG AACAAAAAAA TAACAATAAT GTAAAAGAAG TTTCGAATAG   240

TGTTCAAGAA GATGGTCTTA ATGATTTATA TAGTAATCAA GAAAAGCAAA AAAGCTTTAC   300

TAAAAATTTT GGAGAATGGA AATATGAGGA TTTAATTAAT CCTATAGAGC CTATAATACC   360

TTCAGAATCA CCAAAGAATA AGGCTAATAT ACCAAATATT TCAATTGTGC ATACTCAAAA   420

AAAAGAGATA AAAGAGGAGG ATTTAATCCC TTCTACTAAT GAAGAAAAGG AAGCTGATGA   480

AGCAATTAAA TATTTAGAAG AAAATATTCT TCAAAACTCT AAATTTTCTG AATTAATTAG   540

AGAAGTACGT GTACTTAAAG ATGAATATGC TTTAATAAAC TCTGATTTTT ATGATGTAAT   600

TGAAAGATT CACAATAAAA AAACATCATT AATGGAAAAT TATAAGAACA ATAGAGATAA   660

GATAAATAAA TTAACACTGT TGCAAAATAA TTTAAAGATA AATATTGAAC TTGAGCAGCT   720

TATAAATATG ATTGATATTG CAGAAAATGA AATAAGATCT GCGGCTTTCT TTTTTGACAC   780

CGCTCAGAAA AGGTTAAAAG AAAGTATTAT TAAAAGATTA GAGAGTAAAA ATAATAGATC   840

TTATTATGCA TTAGAATTGT CTAGACAGGC TTTAAGTGAC GCAAGAAGTG CTTTAAGCAG   900

TTTAGAATCT TTTGCTTTTA AAAGAGCTGA ACCAATGGTA AGAAAGAAAA AAATAAAAGA   960

GCTTATTAAA CATGCAAAAA CTGTTTTAGA AAGTCG   996

(2) INFORMATION FOR SEQ ID NO: 96:   ----

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 986 base pairs

     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGGACTATAT ATACTAAAAG GGACTTGTGC TTGTATTCTA TTGGCTAGTT GTTCTTTTAC   60

AAGATGAGCG TCAAAGCGTA CATaGTATTG CCAAAAACAG TCATTTTGAG TAAAGAAATC   120

ATATCCTTAT ATAAGGATGT TAGTATTCCC CCGTTTAATG AkATATGTTC ACCAGTCATT   180

ACCGGATTGT AGCTTACATA TTCCGCTTTT CTATCATAAT AATTGATAAC TGGTCTTTTA   240

GAACAACTAG TATTATAAGT GCGTGTTATG AGTTCATTTT TTGGTTTTAT AAAAAACAAT   300

TGAGGAATAT ATCCAAAACC TTTTAGATCC ATTCTAGGAA ATAACACTAA AAAATTATCT   360

GcTCCGAAAA GGGCAAATAT TTGGGTTATt ACATCTCTTA TTATTCGAGT AATCTCCCTG   420

ATTTCTTcTT TtCAATATCA TTAATTTTTT CCTTGATTTT TTTCTTTtCA ATATCATGAT   480

TGTTAGTAAT TTTATTATTA ATATCTATTT TGTTAGCTGC ATTGTTAGCA ATTTTTTTGT   540

TACTTGTCAT AAGTAATTAC CTTTTGTAAA AATTATGGTG TGCTGTTAGC ATTGTCTgAT   600

TTTGAATTTC TTCTTGTAGT TTTTTTAGAG CCGCACCCTC ATCTCCGCCC ATCCATCCAG   660

GTAGCATCGA TTTtAATTTk GCAAAGAAAT AATtAAGATt AAAAATACTT TtAATGCCAT   720

tAATtAtGGG ATAATAAtGT GTGTTTCAAA CGCAAaGTCT TtAAaGTAAT aGTTATCTTA   780

TAAGAGGTCA AGTAAGGGTC CAAGACAGTA GTGGTTAAGT TTTGAAGAGT TTGCTCAGCT   840

GAGGCCAAAT TACTTGAATA CTCTCAGCAT ATTGACTTTT TTGTAAGGCC GAAAGATTAA   900

AATCCTCGAA CATTTCCATC ATCTGGTAAn TCTAGACTCT AGAnCTACTT GTGCCCCGCT   960

TTGCCAGGCC ATTTGGCATC TTCTAT   986

     (2) INFORMATION FOR SEQ ID NO: 97:

            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 976 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

ATTGAGCACT CCTTTACATA TTCATCAAGC TCGCTTTTTA AAGAATTAAT TTCTCCATTA   60

ACAACTTGCT TGTTTTTTTT ACTACTTGCT TTATTTAAAG CGTCAATTTC GGCTCTTAAA   120

TTTTCTATTT TAGTATGCAT ACTAACAAGC TCAACACTAG AATATTGCTT AAATGCATTT   180

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ATAAATCCTA ATTCTAAATT AGCCCGCTCT AAATCCAATT CGCTTCTAAC TTTCCTAGCG        240

TTAACTTCTG ATCTAAAGGT TTGCGACAAA AGGTGTTCAA AAGTATCTTC ACTAATTGTT        300

ACTCTAGAAT CCTCGCTAAC AGAAGTTTCT CCACTTTCCC ATTTTTGTCT CATTCTCCAC        360

ACATTTACCC TAGAAACTCC CAATTTAACC GATATTTCTC TATCATCTAA CGATCCTTCT        420

CTAAAGTATG CAACATAATC ATtAAAAGAC CTTTTAGCTC TTTTCAAAAC AATTTCTCCT        480

AAAATAACTA AATTAACAAA TTGTTACTCT AAATAGTAAA TCAATTTGTT AATTGTTAAC        540

ATTAACTATT ATCTTATTGA TATCTATTGA CAGGTGTTTG GTATTTTTTT GACTTTTATT        600

GATTTAGAAA TAGCAATTAA CTAATTTATT GAATTTTGCA ACAACTTGAC TATATAAATT        660

AGGGAAAATC TTTTATTGTT TTAATTAGAT CATCGCTTGT AAAAATTCTC TTATCATAGT        720

TGTGkATCCT TATAAATAGT ATATCTTTAA ATTCGTTGAT CATAATTAAT TGATATTGTT        780

TTGAAACTTT TTGATAAATA TGGTTAAGAA TACCATAAAC AGCCCCCAAA AATATCATGG        840

AATCATACTC TCCTAATTTT TTCAAACATT TCTTTAGCAT CCCTTTCTTG TCGCTATAAT        900

CAACTTGCAT ATTTTTGGAA TTTTTATATT TTTnTATTAA ATATTTATTT TTCAGAACGT        960

CTTTAATAAT TTTnTT                                                        976
```

    (2) INFORMATION FOR SEQ ID NO: 98:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 968 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```
GTCAGGCTTT TTACAGAAAT TATTATAATA AATAAAAGCT TTATTCAATT CTCATGTTAA         60

AGAGCTTAAT AAAGCCGCGG GCTTAGCTCA ATTTATTTTA GATAAACTCA CTAAACGATT        120

AAATTCAGTT CAATTTAGAA TTAAAATTAT TTTGTATTTG TTAAAATAAA AGAACCTATT        180

TAAATTCTCT TGTTAAAAAA TTCAAATAAT TTCTACTTTA AAGCTATATA CTAACTTATT        240

ACTTTATAAA ATTTTAATCA TTCTTAATTT AAAAAATACT TATTGAATAT AGAATAAATA        300

ATTGGAGCAA GTGTTATTCC CATTATTAAA ATTACTTGTA TTGTTCTATT ACTTGCAGTA        360

AGTTCGTTTT TTAAAACATT TATTTTATTA TCTAGGTTAA ATATATCCTT TTGTAAGGTT        420

TTTTCTACAC TATCTATTTT AGTATTCAAG CTAGATATAT CTTTTTGCAA AGTTTTTTCT        480

ACATTATCTA TCTTAGTATC TAAACTATCT ATTTTGGCAT TTAAGCTCTT TTCTACATTG        540
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1079

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TCTATTTTGG CGTCTAAACT ATCTATTTTA GAATTAAGTT CATTTTTAAC ACTATCTATT    600

TTAATATTTA AATTCTTCTC TACATTATCT ATCTTAGTAT CTAAACTATC TATTTTGGCA    660

TTTAAGCTCT TTTCTACATT GTCTATTTTG ATATTCAAAC CATCTATTTT TAAATTTAAA    720

TTCTTTTCCA CATTGTCTAT TTTGGCATCT AAATTAGATA TGTCTTTTTG CAAATTCTTC    780

TCTATATCAA TTATTTTCTC TTTTAAAAAT TCAAAGTTGT AATaTCATTA TGCAGAAAAA    840

CAAAATCTAT gCTtCCTgCT AAACCCTATA TTAAAAATTC GTTTTTAATA CCTTTCTAAT    900

GGTTAATAAT GGTTTGGTAA TGGCCTAAAA TTGGTTCCAT AAGGATTAAC CCTTTTAAAT    960

GGTTTATA    968
```

(2) INFORMATION FOR SEQ ID NO: 99:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 954 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```
GCAGGTCGAC TCTAGAGGAT CCCCTTTAAC TAGAATTTTT CAAAATGATA AAACTTTAAC    60

CCGAAATGAT AAAACTTTAA TTTTTGCAAT TTTATTCTCT TGTTTTTTTT AAAACGATTA    120

GAATAATCGT TGAkCAGGTT TATTGATTAT CAATAAACCT GATCTATAAT ATTATAAGCG    180

GTTTTTGCAA GTTTAATAGG AGCTATAATA TCCATGAACA AATTATTGAT ATTCATTATT    240

TTATTAGTCT TTTCATGTAA TTTAAGTAAT TCTGATCAAA ATAATCCACT AAACATGTCA    300

AATAAAGAAA AAATAAGCGA ATATCAAATA AATGAGTCGT CAAACAAATA TTCAATTTTC    360

AAACGAAATT CAAGCGTTAA AAGATACACG TTCAACCATT ATTACTAACC AAAATGATAA    420

TATTAATTCT ACTATTAACT ACCCACCTTA TATTCAAACT ATCTTAAAAA TAGAAAAACA    480

AGTTGACGGA AATATTAATG GGATGACTAA AGAAAGTGGC ACAGAAACTA AAAAGCTTTT    540

AGAAATTCTA AATGGGAATA TTTCTCGATT TAAAGATGCA ATTCAATATG GAGGAAGTTT    600

TAGGGCTAAA GATGTTAGAG AAAATCAAAC CCAAAAAGAA AACAACAAAG ACTCGCATAT    660

TCATGTCGAC GATTTTAAAG AATACATACA TTTAATCATG CCTAGCATTA cAATAATGCT    720

GATAGTAGTA GTAGTTATTA CTATACCAAC TACATAATAA ATGGAGACAA TTTGTkAAGA    780

ATTATTAGCA ACTTATAArA AATCTTTATA AATTACCAAT ATTCTTGACA ATTTTAATAC    840

TATTTTTTTT ATATACTATA ATATTATGAA AAAAAATCAA AAAAACAAGT GCTCAGAAAT    900

AGAAAAAACA CAATTAGAAA TAATAAATAA CCAATCAGAA ATAGAAAAAC AACG    954
```

(2) INFORMATION FOR SEQ ID NO: 100:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 946 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```
AGAAGAAAAT AAATTATACA GATCTTCTGT ATCTTTTAGA TATTTTTTTT ATGATGAAAA      60

TACAAAAAAG AAATTAGGGT ATAAAAAAAT AATAACAATT TTCAATTTGC TTGATAAAGG     120

AAGTGATGCA ATAAAGTTTC CCATATTTAA TGGAGGATTA TTTGCACAAG ATAAGGTTAA     180

ATATTTAAAT AATGAAAGTT TACTCAGTAT TAGTGAGATT GAAGAAATAT TAGTCAAAAT     240

ACTTTTCTTT GAAGAAAAAA ATATTAAAGA TAAAAAATTT GTAAAATATT CAAGGCTAGA     300

TCCTAAAAGC TTTGGAGAAT TATACGAAAC TCTACTTGAA TATGACCTAA GAATTGCAGA     360

TACTACTGTT CATCGTATTG TTGAAGACGG GATTTATCTC ATTCGTACTG AAGAAGAGCT     420

TGAAAACAAT AAAGTAAACA AAATTGCTAC ATATCTTAAA GGGAATATTT ATCTTACATC     480

TAGATCACTT GATAGAAAGA AAAGTGGGGC ATATTATACT CCAGATGATT TAACTGATTT     540

TATGGTTATA TCATCAATTG AAGAGCAGCT TAAAACCAAG TCCCCTTTAG ATATAAAAAT     600

CATTGATAAT TCTTGTGGAT CAGGGCATTT TTTAATTTCT TGTCTAGATT ACTTAACAGA     660

AAAGGTATGG TACGAGCTAG ATAAATTTGA AGATGTAAAA AAAGAGCTTG ATAAAGAATA     720

TGGGATTATT CTTAAAGAAA GTGAGGAGTA TGATATTCAA GATAGTATAA GTAAAGAATT     780

GGTGCTTAAA AGGATGCTGC TAAAGAGGTG TATTTATGGT GTTGATATTA ATCCTATTTC     840

GGTTGAAATT ACTATGCTAA GTTTGTGGAT TAATACCTTT ATTTTTGGAA CGCCACTAAG     900

CTTTATTGAG CATCATATAA AAACAGGAAA TGCTCTCTTG GGATAT                    946
```

(2) INFORMATION FOR SEQ ID NO: 101:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 913 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```
CTTTGACTCA AAACTTTACC CTTTAAATTG CTAACTTTAA CTTGAAAATA CTAAACTTTA      60
```

1081

ACCCGAAATA ATAAAACTTT AACTAGAATT TTTCAAAATG ATAAAACTTT AATTTTTGCA   120

ATTTTATTCT CTTGTTTTTT TTAAAACGAT TAGAATAATC GTTGAkCAGG TTTATTGATT   180

ATCAATAAAC CTGATCTATA ATATTATAAG CGGTTTTTGC AAGTTTAATA GGAGCTATAA   240

TATCCATGAA CAAATTATTG ATATTCATTA TTTTATTAGT CTTTTCATGT AATTTAAGTA   300

ATTCTGATCA AAATAATCCA CTAAACATGT CAAATAAAGA AAAAATAAGC GAATATCAAA   360

TAAATGAGTC GTCAAACAAA TATTCAATTT TCAAACGAAA TTCAAGCGTT AAAAGATACA   420

CGTTCAACCA TTATTACTAA CCAAAATGAT AATATTAATT CTACTATTAA CTACCCACCT   480

TATATTCAAA CTATCTTAAA AATAGAAAAA CAAGTTGACG GAAATATTAT TATTAATGGG   540

ATGACTAAAG AAAGTGGCAC AGAAACTAAA AAGCTTTTAG AAATTCCAAA TGGGAATATT   600

TCTCGACTTA AAGATGCAAT TCAATATGGA GGAAGTTTTA GGGCTAAAGA TGTTAGAGAA   660

AATCAAACCC AAAAAGAAAA CAACAAAGAC TCGCATATTC ATGTCGACrA TTTTAAAGAA   720

TACATACATT TAATCATGCC TAGCATTAAC AATAATGCTG ATAGTAGTAG TAGTTATTAC   780

TATACCAACT ACATAATAAA TGGAGACAAT TTGTTAAGAA TTATTAGCAA CTTATAAAAr   840

ATCTTTATAA ATTACCAATA TTCTTGArAA TTTTAATACT ATTTkgTTaT ATACTATAAT   900

ATTAAGAGAA AGA   913

(2) INFORMATION FOR SEQ ID NO: 102:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 910 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TCGCTATnnG AGCTCGGTAC CCTGATAAGG CGAGTGTGAC GGGGATTGCT AAGGGAATAA   60

AGGAGATTGT TGAAGCTGCT GGGGGGAGTG AAAAGCTGAA AGTTGCTGCT GCTGAAGGGG   120

AGAATAATGA AAAGGCAGGG AAGTTGTTTG GGAAGGCTGG TGCTGGTAAT GCTGGGGACA   180

GTGAGGCTGC TAGCAAGGCG GCTGGTGCTG TTAGTGCTGT TAGTGGGGAG CAGATATTAA   240

GTGCGATTGT TAAGGCTGCT GGTGAGGCTG CGCAGGATGG AGAGAAGCCT GGGGAGGCTA   300

AAAATCCGAT TGCTGCTGCT ATTGGGAAGG GTAATGAGGA TGGTGCGGAG TTTAAGGATG   360

AGATGAAGAA GGATGATCAG ATTGCTGCTG CTATTGCTTT GAGGGGGATG GCTAAGGATG   420

GAAAGTTTGC TGTGAAGAAT GATGAGAAAG GGAAGGCTGA GGGGGCTATT AAGGGAGCTG   480

GCGAGTTGTT GGATAAGCTG GTAAAAGCTG TAAAGACAGC TGAGGGGGCT TCAAGTGGTA   540

CTGCTGCAAT TGGAGAAGTT GTGGCTGATG ATAATGCTGC GAAGGTTGCT GATAAGGCGA   600

GTGTGAAGGG GATTGCTAAG GGGATAAAGG AGATTGTTGA AGCTGCTGGG GGGAGTAAAA   660

AGCTGAAAGT TGCTGCTGCT AAAGAGGGCA ATGAAAAGGC AGGGAAGTTG TTTGGGAAAG   720

TTGATGCTGC TCATGCTGGG GACAGTGAGG CTGCTAGCAA GGCGGCTGGT GCTGTTAGTG   780

CTGTTAGTGG GGAgCAGATA TTAAGTGCGA TTGTTAAGGC TGCTGGTGCG GCTGCTGGTG   840

ATCAGGAGGG AAAGAAGCCT GGGGATGCTA AAAATCCGAT TGCTGCTGCT ATTGGGAAGG   900

GTGATGCGGA   910

(2) INFORMATION FOR SEQ ID NO: 103:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 888 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AACATGTAAA AGAATAAGCA TTAACTCGCG CATTCTTTGA TTTAAAACAA CCACCCGAAC   60

TACTAAAAAC CTTATTTTCA ATCGAACTCA TTGATTTTGA ATATTTTTTA AATTTTAAAA   120

GAACATCGTC AAGTTCTTTA ACTGAATCTA AATAAGGATC TTTTGCCTGT ACTTCTTCAG   180

CCTGTCTTGT TTGACGTTTA GATCTAGGAG CAACTGGAAT TTCTGATTCT AGCCCTAATT   240

GTGGATTATC ATCAACATTA GGAGCTTTAG CTTGCCCTTT GCCTTTTAAA GCCATAATTT   300

AATTACCTTT TAAAGCTCTA TTCCCAAAAA CACTAGCAAG CACTATAGAT AACTCTTCGG   360

TTAATTTATG TACTTTTGAA AGTGCTATAG CATTAACAGA TTTATCATTT CCCCCATTCT   420

TTTCAAGCTC TCCTTGTGCA TTAAAATGCA GCTTATCACC TGGGTTTACA CCATTTCCAT   480

TTTTCTTAAA TGTTAAATAC CCCGTGAAGT TATTTGTAAT TGGAACTACA GTTGCCATGC   540

CAGTAAACTC ATCTATATCA GTGCATATTC CGTACAAGTC ATCCCCACCA CCAGCCTCAA   600

CTTCTAGTTC TGTTGTACCA TCTGCACTAA AACTAAGCTT GACTCCACGC TTGTATGGAT   660

ACCCTTTAGC AGGATAATTT TCTATTTTGT CTTTACTACT AGTAAAAACT CCATCCGAAT   720

TGGAGTAAAT TAGATTTTTA TCTCTAAAAT CTACAGAATT ACTAAGCAAA CCAGTATCTT   780

GCTGAGGATT TTTCATTAAT GCTTTAATTT CTGCAACTTT TTTATCAAAC TCTTCTTTTA   840

TTTTTGTAAT ACCATCGCTC ATTAAAAACT CCTTTAAGCA ATACTGGT   888

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 883 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```
GATAGTAATT AAGTCCTACA ACCAATAGTG TTACTTTGCA TTAATTTGTT CTTTCCTTAT    60

CGATAGGTCT CTTCCTTCCT GATTGAATTT CAGATCATTA GATATTTTGA GACTTTCTTC    120

ATCAGAATTA ACTCAAGTCA ATGCATTGAT TGATTTTCTC ATTTAATGGA GCTAGTGCTT    180

TATTTATTGC TGGGGTTAAT GCACTCTCAA GTCTTTCCAT ATTTGCTGTA TAGATTAATT    240

TmTAATGAGA ATACAGCTCA TAAACCAAAA AGAATCCTTT ATGTGCAATT TCATCAAATT    300

CATCTTCAAA TTTAGAAAAT ATATCAATAA GGGTTGATAA AGACGTAAGT CCAAGCTCAA    360

CATTATCTTT GGATAATTTC ATAAGTTAAT CTCTTTTTTT AATGTGATTT TTGCCATTAC    420

CATTGCCATT CTTAAAAATC TTGCCTATTA CAATAGTCAA TATGTCTTTT AATAAAGGCT    480

TGAGAAGAAT TAACACTCCT AAAACCAATA CTGTTACAAA AATCATTACG GCTATAAGTT    540

TAATTTCATT TAAATTGATA AGAAGTTCTG TTAATTTAAT AGTATCCATT TTTTAATCCT    600

TTATTTTAAT TTTTTATTTG TATATACATT ATATCAAAAT CGTAATTTTT GCTAAAAAAG    660

TTTGCAGCTT TTAAAGCTGC GGGATGGGGC CCCCTGATAG GTAGGCTCTT TTTTGAATAT    720

ACCATCCTTT ATACATGGGA AATCTACTAG ATAGTCCTTG GGGGAGCGTC TGrTTGCTCA    780

TAAGCCATAC TTGTTTCACT TTCATCGGAA TATCTTAGAT AAAGTACTTT ACTCTCGCTA    840

TTACTGTAGT GTTCTGCGTC AAGCTCAATA TCAAGGTAAA TGG                      883
```

(2) INFORMATION FOR SEQ ID NO: 105:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 857 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```
CTATTAATTG CCAAAAAACT AAACCAAACA ACACTTAAAA GGAGAGTCTT ATTGTGATAA    60

TGAGATATAA AATGAAAATT TTAACTAAAA ATAAAACTTA TGAATATCCG CTGAGAGTAC    120

TTCCCGTCTA TGAATGGGAT AAAGTGCTAG GATTTAATCA AAGTGACGCT GTTTTAAAGC    180

TTAATGAGGT TAAATTCTTA AGAGAAATCA CAAGCTTAAT GATAAGTCCA AAATTTTTAG    240
```

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ACGAATTCTA TGTGATTTTG GATCAAAATA GAGAATTTAT TTCTTATTAT AAGGACTATC      300

TTGTTGCAAT AATTTACACT GCACAATTTA ATACTTTTCA TTTAGACAAT AATCTAAAAA      360

AGCCCGCTTT AGTATATTTG AGTGAGTATG AAAATAATGT TGGTGATTTT GTTGCTTTtG      420

ACTATATTAA TGAAAATTTT GATTATGAAA AAGTAGCCAC TTCGCTTTCA TCAATTACAT      480

CAAATTCCAA TGAGCTGGTT GCTAAATGAG CAAAAGAAAT AGAGATATTG ATAAAGCTAT      540

TGCAAGTCTT GATGAGACTA GAAAAAAATA TTTTAACTTG CTTGACGAGA TTAAGAACGA      600

TAAATACTTT TTCCCAGTAA TTATGAATAT TTGCTCATAC TACTCGGTTA AAAAATTGCC      660

TTATGACGAG CTTTTAGAAG TCAATAGACT TGCTGAGATT AAATTAGAAA AGAATTGTA       720

TGAATTAATT TTAAGCAAGT GAGGACTTAG TGAGCGACAA ATTCACCATT AAAtTTAAAG      780

GtATTCyTGA TCaTGCTGCA ACAAAAAGG GCCATTGAAC CAGGATATTT CTAAAATGGn       840

AAAATTATCn TAAACCT                                                     857
```

(2) INFORMATION FOR SEQ ID NO: 106:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 846 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```
AGTTGTTCTT TTGCGAGATG CGCGTCAAAA CGTAGCATAG TATTGCCAAA AACAGTCATT      60

TTAAGTAAAG AAAGCATATC CTTATATAAG GATGTTAGTA TTCCACCGTT TAATGATATG      120

TTTTCACCAG TCATTACCGG ATTGTAGCTT ACATATTCCG CTTTTCTATC ATAATAGTTG      180

ATAACTGGTC TTTTAGAACA ATTAGTATTG TAAGTGCGTG TTATGAGTTC ATTTTTTGGT      240

TTTATAAAAA ACAATTGAGG AACATATCCA AAACCTTTTA GATCCATTCT AGGAAATAAC      300

ACTAAAAAAT TATCTGCTCC GAAAAGGGCA AATATTTGGG TTATTACATC TCTTATTATT      360

CGAGTAATTT CCCCGATTTC TTTCTTTTCA ATATCATTAA TTTTTTCCTC GATTTTTTCT      420

TTTCAATATC ATTAATTTTT TCCTCGATTT TTTTCTTTTC AATATCATTA ATTTTTTCCT      480

CGATTTTTTT CTTTTCAATA TCATGATTGT TAGTAATTTT ATTATTAATA TCTATTTTGT      540

TAGCTGCATT GTTAGCAATT TTTTTGTTAC TTGTCATAAG TAATTACCTT TTGTAAAAAT      600

TATGGTGTGC TGTTAGCATT GTCTTGATTT TGAATTTCTT CTTGTAGTTT TTTTAGAGCC     .660

GCACCCTCAT CTCCGCCCAT CCATCCAGGT AGCATCGATT TTAATTTTGC AAAGAAATAA      720
```

1085

TTAAGATTAA AAATACTTTT AATGCCATaA TTATGGGATT AATAAGTGTG TTTCAAACGC   780

AAAGTCTTAA AGTAATAGTT ATCTTATTAA TGAGGTCAGT AAGGGTCCAA GACGTAGTGG   840

TTAAGT   846

(2) INFORMATION FOR SEQ ID NO: 107:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 840 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CAATGAAATA GTTAGAGAAA TTAAAAATGT TATTAAAAAG CACAATTTGG AGCTTGATAT   60

TGAGCAATAT CCAATTTCTA TAGAGGGTCA ATATGGCATA GTTGATTATA TTAGGACTAC   120

ATTCTACAGT ACAAGTACTG GATATGAATT TTCTTTTGAT ACGCGAATTC CTACAGAAra   180

TTtACAATGG aACAATGAAA ATGGGTCTAA AGTTACAAAT ACAGTGTATC AGATGTTTGG   240

TTCAGGCATT ACTTATGTCA AAAGGTATGC TTTAGTTGCA GCTCTTGGTA TAGAAAGTGA   300

AATAGATACT GATGCAGCTC CTATTTACAA TAACCACGAA AACGAAAATT CTATGCCTAG   360

CAAGCAAGTT AGTGTTAATC AAAAGCAAGA ACAAAAAGA GAACAAAAAC AAGAAAAAAA   420

TCAACTAAAC AACTTTAATA AAAACTTAAA ATCTGGCAAG GCTTATTGCT ATGAAATTTT   480

TAGAGACGCA CTGTTTAATA TAAAAAATTG GGTAAATGAA GGTGAAGAAA AAAATAATAT   540

AAATGCTCTT ATTCGGGCAT TATGTACTGA TAATGATGAT GCTTTAGAGG ATCTTTTTGA   600

AAAGAATGCT GAGCTTAAGA ATATAGAATA TTGGGTAAAT ATTCTAAAAA AATATTTCAA   660

TAAAACCnAT AGATTTGATG ATCTAAATAA GCTnAAAGTT TTTATGTCTG ATAATCGGGA   720

TGTTTATAAA ACAAAAAnTA TTAAAATTCT TTTGCATGTT AAAAAAAAAA AAGACAATTT   780

AATTATATnT TTGCCAGTGT TGCCATATTA AAGCCCCCCA ATAAGGGGGC TGTTTAnATT   840

(2) INFORMATION FOR SEQ ID NO: 108:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 814 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGACTTT GTTTTATCTA CAATAACTTA TTTTAGTTTG AAAATTACAA GCAAGCCTGA   60

AACCATTCAT TATCCCTATG GACACAAACT AATGGAAAGC TTAATAGCTT TTATCATGGG 120

AATAATTATA CTTATGACAG GATTTACACT ATTTCTAAAT ACAACCGGAT TAAATAAATT 180

TATCACTCTT GGGGGAGAGT CTGGATTTAA TCTACACATA CACCAGAACA AAAATAAAAA 240

TGATACTATA TATGAACATG ACCATTGCCA TTCACACGAT CACGATCACG ATCATAACCA 300

CGACCACAAC GAAGAAGACA AAAAAAACAT ACTAGAAATA TTTCAAATA AATGTCTAGA 360

AGCAAAAGCA AGCTTTCGAT AAAACCCGAA GTTGTTTCGC TAAAGTGACA AGGATTAAAC 420

AGGATTGTAT TTTTCAGCAG CCTATTTTAT AAACGATCTG CATTTAGTAA ATAGTTTTTA 480

GTTAGGAAAT AATGTAGGAT TACTAAGTGT GATGTCTGAG AGAAGGGACA AGTATTGTAG 540

CGAGCTTAAA TCCTTATTAT CGTTGGCCAG TAATTTAGAG GTAGGGGATC GGGATAAAGG 600

ATTGGCCAGT TTATAAGTTG GAGGGAAGGG CAAAGGATGC CTTAAAATCG GTAATCGCTC 660

CTTAAGGTTT AGGGTTAACA AGTTTGGCCA CCAATTAACC TCCAAAAAAA GGCCAGGCAA 720

AAATACCCAT TAAAGGCAGG ATTTCCGGTT TGGGAATTGG CCCCGGACCA CCTCCAAAAG 780

GGCCATGGAA GGTTTGGGAA ATTGGTTAGG TAAA 814

(2) INFORMATION FOR SEQ ID NO: 109:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 808 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGCAAAACCA GTTCTATTTT GTTCAAAATC AATATTCGAC TCTTCAGAAT TTAGTTTTAA 60

ACTTTTGATT TCATATTTGT TTTCAAACTC TTCAGTTGAT TCAAATGCTA TTATCTTAGC 120

TATAGGTACT TCTTGACCGA ATATTTTATA GTTATTGTCA TTAATGCTAT AATTAAGTAT 180

AGCTAAAGGT AAGCAATGAA TAAGTTTTGA ATCGGATGGG TGAAAAAATA TAAGAATACT 240

TAAGCTCTCT AAGATTTTCA ATTAAATTGT TATTTTTATC TTTTATATCT TTTAAATCAC 300

CAGATTTTGC CCATGTAACA TAACCACTTG CAAGTATTTC AAATGCCTCT CCTTCTTTTA 360

TTTCGTTTAA TTCGGGTTCC TTAAAGGTAA GACAAATATT GCTATTACTC TCTTCAATGG 420

GCTTTTTATC ATATTTTATA ATATTTCCCT CTTCAATTAT CTTAAAATCC AAAACCTCGG 480

TTTTGATACT GTTGATTTTT GAAGATTTTG GTGTAGTCAA AAAGCATGAA TAAAATAATG 540

GTATATATAA AAATATATTC AAAATACATA TGTTCTTTTT CATAAAATTT TTCCATTAAT 600

TGTATTTCTT TCTATTTCTC TCTTCACTTT TAAATATTGT TGATAAGCAG TGGGTCTAGG   660

CATAAAACGA TCATACTCAG GGCTCCCCTC TTCGCCAGAA TACTTAATAT CTGGAGAATA   720

TAACTCGCTT ATACATGAAT ACAGCCAATA AACTTCACTT TTAAATTTAT TATTCTGCTC   780

ATTTTTTACC CTACCAAACA ACTTAATC   808

(2) INFORMATION FOR SEQ ID NO: 110:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 804 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TGGGAAACAT TATATCTAAC AACCCCTAGT GGTACTTTAC TTGAGGGGGA CATAGAAATT   60

GATGGCCTCA ATTCAACTGG ACAACGAAAA TCCTACAAAA TATCGCTAGG AAAAAGAAAA   120

TATGTTTATA TGAAAGTAAA GTATAAACTT GACCTTAAAA ACTATCTCTA CTTAAACATA   180

GACTCTCAAA TTAGAGACAT TTATTCTAGG ATTATTTCAA ATAACTATTC TGATATGGGA   240

ATTAGCTTTG AATATCAAGA CTTTTTTGCT CCAGTTAATG AAGTTAAAGG AATTAAATTT   300

ATGGAAATAA GTGCCTGTAT TAAAGACACA GACACTGAGA GTATTGCAAA AATTACTGAT   360

AGCGATTTTA AAAAAAATCA AGATATTACT ATTACTGATG ATACAATGCT CCTTTTCAAT   420

ACTACAGATA GATTGCTTAT TGATATTGAT AGTTAACAAA TATGAAAATA CCTAATTTAT   480

TCAATGGCAC TGAAGTTCAT AAATTTATAC TTACAGAAAC AGAATATGCA CAAGCATTGC   540

TTAATGAACT CAAGTCTCTT AATTCTAACT TCCTATCCAT TAATGTAATA GAAAATATAA   600

AATCAAGATA TATTGCAATA TGGATATCTC AAGTTTTATC TATCTTTTAT GCAAAAACTC   660

AAACTTTACA AAGTATTACA AGCAATATTA ATAGCGTTAT TTTTGCTTTA CGCCATATTG   720

GTACTGATGA GTCGTTTAGA CTAATTTTCA aGGCCTTTTa AATGTGGACA TGAAGTTACT   780

ACTCCTGAAG CGGGGGTATG GAAA   804

(2) INFORMATION FOR SEQ ID NO: 111:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 800 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```
GCGTGAGATG TTAATTTTTA CCnGCTTTAA AGCAGAATAG TCCATCCCCA TGAGGAGCAT      60

AGCTTAAACT nCCCCTTAAG GTTTTTAAAA ATATCAAAAA CCTTnGTTTT TGTTCATCAA     120

TTCCATCAAC AGTGATAAAC GTTATTAAAT ACCAATTCAA AATTATTGCC TAATCTTAAA     180

yCCATACTAG TAATTATACC ATATTTAGCA AAAATTACTT AAACAAACTA TTAATATCAG     240

AATTAATTTG AGCGGTTGCT ATTTTTAAGC TTGATTCGTC AATTACTGAG TCCCCTATAA     300

TTTTTATACC ATTGATAGCA CTAACAATAT TATCTAGAAT TTTTTTTAAG CTAGTTGTTT     360

GGTTTGCTAT TTCAATTTTA TTATTCGCTC TAATTTTAAC AGTATCAGAG ATTAGATTTA     420

AAGTCTTTGG GCTAATTGCA CTAAGTATAT AAAAATGATG TTTGTCAAAG TGAATATCGT     480

TATTTTTATC AAAAATATTA ATGCTTGATT GAAGTAGTAA AACGCAATCA CCTTTTGATA     540

GTTCTAAACT GATATTAGAG ATATTTTTTG TGTGAATTTC TAAATCTTCA AATTCGGGTA     600

TTGTAACAAT AGCTTCTTGA GTTTGATGTT TAAACTCCTT TACAGTGCCA ATTTTAATTA     660

TAAAAATGTT TGAATAAATC CAATTTTTAA GGTCTTCTTG AGCCAATGCC TGGCCATAAA     720

GGCGTTGATT CATTCtGTAA ATTTCATAGT CTTCaTTCaT TCtAATTCyA GTCCCCTTTA     780

tTTTTTACgt TTTGTATTAG                                                 800
```

(2) INFORMATION FOR SEQ ID NO: 112:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 798 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```
GAAATAGCTT TTTAAGTTTT CTAAATCATC TTTAATATCA ATAACTTCTA TAAAGTATTA      60

ATGATGAATT TTTGGGAATG TTTTATGGAT TTAAAAGATT AACAAGACCA CTTTTTTTAA     120

ATACGAAGAT ATTATTACAA AAACTATCAA AACTGTACCC ATGTATAAAA TTCATTACAT     180

AGAATTTAGA TTTAAGAAAG GAAGTGTTTT TTGTTATATA AAAGCAATTC ATGTTTTAAT     240

AAAAAAAGAA AAATTTAAAA AAAATATGCT CAAAGTCTAT TAGAGAGAAT AATTAATCTA     300

GAACATAAAG TATTAAAGAT AAAGCAATTT TTTTAAAAAA TATATAAAAA TCGAAACAAA     360

AAATTAAAGA TATAGTAAAA TTGTATTTGT AGCAATATAC TTGTGCTAGA GGCTATGAAT     420

CTCTAAAGAT TTTAGCAGGG GAGAAAATAT GAAAAAAGT TTTTTATCAA TATACATGTT      480

AATTTCAATA AGTTTATTAT CATGTGATGT TAGTAGATTA AATCAGAGAA ATATTAATGA     540
```

GCTTAAAATT TTTGTTGAAA AGGCCAAGTA TTATTCTATA AAATTAGACG CTATTTATAA   600

CGAATGTACA GGAGCATATA ATGATATTAT GACTTATTCG GAAGGTACAT TTTCTGATCA   660

AAGTAAGGTT AATCAAGCTA TATCTATATT TAAAAAAGAC AATAAAATTG TTAATAAGTT   720

TAAGGAGCTT GAAAAGATTA TAGAAGAATA CAAACCTATG TTTTTAAGTA AATTAATTGA   780

TGATTTTGCG GGATCCGT   798

(2) INFORMATION FOR SEQ ID NO: 113:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 798 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AGCTTTTGCA TAATAATTTT CATCAAATAA TTCCCATATT AAATCCTCCC AAATATCATT   60

AATTTTTACT TACAGCTTTA TTTCCAAATA CTGCTACTTT TATTAAATAA ACATCGTTAC   120

TAATTTGTTT TGCATCAGAC AACGCTATTG CATTAATAGT TGCCTTATTT GGTGGTGCTC   180

CAGTCACCTT TTCAAGAGCA CCGTCTTTAT TAAAAACAAG TTTGTCTTTT ACTTTAAGCG   240

TAGAATCTTT TGCTACTAAA TAACCCTCAA AATTATTTGT AATCGGAACA ATAGTGGCTG   300

TTTTGCTAAA CTCATCTATA TCAATGCATA TTCCGTATAA ATCATCTTCA CCACCAGCCT   360

CAACGTGGGG TTCATAGTGA ATTTGATCAG CTTTTTCCTC TTGAATAACT CTTTTTACCC   420

CACGCTTATA TGGATACCCA GAAAATGGAT GATTTTCTAA TTTGTCAAAT TTGCTGGTTC   480

TAGTGCCTCC AGAGGCAAAA AATTGTATGT TTTTATCTCT AAACTCTACA GAATTGCTAA   540

GCAAACCAGC GTCATGCTGG GGATTTTTCA TAAACTTTTC AAGTTTACTT CTCTTCTCTT   600

GaTAATCTTT TACTAATTGC GTTGTGTCTG cCATTTGTTT AACTCCTTTT ATTGcCCAAG   660

GgCkAwCCrC CAGCTtCAGG TGTTACTGTT TTCTCAAGGG CCTCTATTGG CCAAAAATTG   720

GCAAACTTTT TTTTTAAATT CCCAAAAAAA AATTTTTAAA AATTTAAAGG GAAAAATTTA   780

AACCCTTTCC CCTTTTTG   798

(2) INFORMATION FOR SEQ ID NO: 114:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 783 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
GGACTCAAAA CTTTACCCTT TAAATTACTA AATTTAACTT GAAAATACTA AACTTTAACC      60

CAAAATAATA AAACTTTAAC TTGAATTTTT CAAAATTACA AAACTTTAAC CCAAAATGAT     120

AAAACTTTAA TTTTTTGTAA TTTTTACATA AAAGTGTTAA CTTTAAAATC CCAAACTTTA     180

TAATTTTGGG AAATTATCAA TACTTTTTTA ATTTATTCTT TATTTTCAAA ATAATCTTTA     240

TATACTTATA TATTATGTAT AAGGCTATAA AAGAACAACA AGAAATAGAA ATAGATCATG     300

CATGCAGAAT ACTTATTCTT ACCGCAACAA TATTTGAAAT AAATTCAATA TTCGAAAATT     360

ATTATCAAAA AACTCTACTC AAAAGTATA ACGAAAATCT CAAAAACAAA AATCTACCTC      420

CTAGTAATAT ATCAACAATG AAAAAATACT TAAATCAATT AGAAAAGAA ATAAAAATCA      480

TAGCAAAATT CTATTTTAAA AACGATCAAT CTCTAATTTA TTGCAAACTT AATTATACCC     540

TAGAAAAAAT TTGTTTAAAA CTAATAAAAT TCTACAAAAA ATTCTACAAA GAATTAAAAC     600

AATTTACACA AAAGAACATT ACTACTTAAT TGTAAATACA TTATAAAATA ATCTTATGCA     660

AATATTTAGA AATACAAATT GTAAAGATAT ATATTTTTAT TTAAATAAAT AATAAAAATT     720

GCTGGCACAC TAATTTGGAA AAATCTTTAA AAGAnATACT AGGTATGAAT AGCnAAAATA     780

AGC                                                                  783
```

(2) INFORMATION FOR SEQ ID NO: 115:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 768 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```
TTCTATATAA ATATTTTGTA ACTTTTTTGC TTATTACAGA CTAAGCCTAA ACGTCCTACA      60

ACCCCATAAA TGCAACGCTC TGCAGCTTGA CACATTTAAA GTTTGGGCTA CTCCCTTTTC     120

GCTCGCCACT ACTAAGGGAA TCTCTTTGAT TTCTTTTCCT CAGGGTACTT AGATGGTTCA     180

CTTCCCCTGG TATCGCCTCT ATTATTTAAA TAATAGATAG CTAGCATCTT GCTAGCTGGA     240

TTACTCCATT CGGTAATCTT GGGATCAATA AATGTTTGCT TCTCCCCCAA GCTTTTCGCA     300

GCTTACCACG ACCTTCTTCG CCTTAAAGCT CCTAGGCATT CACCATAGAC TCTTATTACT     360

TTGACCATAT TTTTATCTTC CATCTCTATT TTGCCAATTT ATTTATACAA CATAAAATAA     420

TATATATCTT TGTTTAATAC ATGTCAATAT ATATTTTATT TTTTATGTTA TTTAAACAAC     480
```

ACATTCAAAA ACACCAATAT TTAAAAAACA TAAAAATAAA ATCAAAGTTT AAAGTATAAA   540

AATAAAAACC CTGGCAATAA CCTACTCTCC CGCGAACTCG CAGTACCATC AGCGAATAAG   600

AGCTTAACTT CTGTGTTCGG AATGATAACA GGTGTTTCCT CTTTTCTTTA ACCACCAGGG   660

TTTTTACAAG GAAGACAAAA ATATgGcCAA AGATACGGGT AATTAGTATT AGTCAGCTTA   720

ATATATTGCT ATACTTACAC TTCTAACCTA TCGACCTGGT ATTCTTTC   768

(2) INFORMATION FOR SEQ ID NO: 116:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 765 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CTTTACGCCT AACTTACCCT CCACGTGTAC AACCCCTTAA CAACCCCTTA ACTTACCAGT   60

GACCCCCTTA ATATGGTAGT TATGGGGGAA CGCTTAGAAT AAAAAAGTCA TCTACGACAC   120

CCCCGATCAT AGACCTGACT CTTGTTATCC CAAATCACTT CAGCGCCCTC GCAACTTATG   180

GGAAAAAGTT CCTAGAAAGA TGTATAGAGA AGTGGAATCA AAGTAATAGG CAATTCGCAA   240

GTGAATAAGG GAGAAAGGAT TTCCTATGTT ATAGGGAGAC GCTAGACATA GTGCTTGCGA   300

GACTGGATTG TGCTTGATGG ATAGAACCTA GTTTAGTGTG TACATCCAAA AAATGGACTA   360

AATCAATAGT ATAAGGCGAA TTGCCAGCGA TGAGGTCTGA ACCAAATTGC CTCACATCAG   420

GCGATAACAG TTACTACTAA CAGTTGCCAC TTCGGCTACT CTATCTTGCG TGCTTATTGT   480

AGCACTCTGG AGGTCCTGTT GTTAAGCCAG CATTAGCACA GCTCCTCCAC TGCGGGTTGC   540

GAGTATAGAG TAGTCCTAAC TGGCAAGGAT TCCCCCTCTG GTTGCTAGAG GTCGAATTAC   600

CCACCCAACA ATAGTTGCAT TGTTGGGGGG GTGGGTACCT ACTACTCGGC ATATACTCCC   660

CCCCTTTCGA GACCTCCCTC GAGGGTCGAG GGAGCATTTG ATCATAGACG TTCATCCCAG   720

ACATGGCCTT TCGGGTTTGA CGTCTCGCGA CCCCCCTTCG GGGAC   765

(2) INFORMATION FOR SEQ ID NO: 117:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 755 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

●

1092

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GAGCCATTAT TGGCTCCTAT TTTACTAGCT GCACTTGAAA TTCTTTTCTT TTTTAGGAAC       60

AAATAACGCT CTTTAAATTA AAAGGCATAA TGCTATATTG TATTCTAAAT CATATACAAA      120

GGACAGTTCT TTATATCATA AGTGCAAAAA TAAAGTCATA AATTCAATAA AAAGGAGGAA      180

AACTCTTCTA GAGTAGTAGA AGAGCAACCA AAAATTAATG AAAATTTTTC TACACAAGAA      240

TCTATACAAA AACTGCCCCT TTACTGCAAC ATACAAACG TGAATCTTGT ATATTACAAT       300

AATAGATAAT ATTATTGCAA CAATCCTAAA TTACAAATAC AGAATATGTT ATTAGCCCCA      360

AAAAGGGGCT AATACATTTA CTTTAAATTA CAAGTTATTC GAACCATAAT TGTTCAATAT      420

TAATTTCAAA TCTTTTCTTA TAGCAAGAAA TTTTTCATAA ATCAATATTA GATAATCATC      480

AAAATTGCTT TTATCAAGCA CATACAAAG TTTAAAAAAA TCTACATCAT CAAGACATAA       540

ATAGAATATG AAAACCTTAT TTTCAAACAC ATTATCACCC AGCTTTACTT TAATTTTACG      600

AAAAAGGTTG ATTAATTCTT TAGACTTTTT TGGCCCCAAA TTAAAAAAAA ATTCATTTAA      660

AATGTTTTGA CTTTTAGGCG GAGACAATAT ATTTATTGTC TCCGCATCAT TTTCTATATC      720

TAAGAATCGA CTCATAGGAA CTTATAAATG ACTTT                                 755
```

(2) INFORMATION FOR SEQ ID NO: 118:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 753 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```
CTCAGCCAAG ATACTGGTTT GCTTAGTAAT TCTGTAGATT TTAGAGATnA AAATCTAATT       60

TACTCCAATT CGGATGGAGT TTTTACTAGT AGTAAAGACA AAATAGAAAA TTATCCTGCT      120

AAAGGGTATC CATACAAGCG TGGAGTCAAG CTTAGTTTTA GTGCAGATGG TACAACAGAA      180

CTAGAAGTTG AGGCTGGTGG TGGGGATGAC TTGTACGGAA TATGCACTGA TATAGaTGAG      240

TTTACTGGCA TGGCAACTGT AGTTCCAATT ACAAATAACT TCACGGGGTA TTTAACATTT      300

AAGAAAAATG GAAATGGTGT AAACCCAGGT GATAAGCTGC ATTTTAATGC ACAAGGAGAG      360

CTTGAAAAGA ATGGGGGAAA TGATAAATCT GTTAATGCTA TAGCACTTTC AAAAGTACAT      420

AAATTAACCG AAGAGTTATC TATAGTGCTT GCTAGTGTTT TTGGGAATAG AGCTTTAAAA      480

GGTAATTAAA TTATGGCTTT AAAAGGCAAA GGGCAAGCTA AAGCTCCTAA TGTTGATGAT      540

AATCCACAAT TAGGGCTAGA ATCAGAAATT CCAGTTGCTC CTAGATCTAA ACGTCAAACA      600
```

1093

AGACAGGCTG AAGAAGTACA GGCAAAAGAT CCTTATTTAG ATTCAGTTAA AGAACTTGAC 660

GATGTTCTTT TAAAATTTAA AAAATATTCA AAATCAATGA GTTCGATTGA AAATAAGGTT 720

TTTAGTAGTT CGGGTGGTTG TTTTAAATCA AAG 753

(2) INFORMATION FOR SEQ ID NO: 119:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 747 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TGATTTTAGC TGTTTTGTAA mCCAAAAGTG GATTATAATA ATTGGGCCTA CTAGTCTGAA 60

TCCTAGAGTC AATAAAACTT ACACTAATTG TATCTTGCGG CAATTTCGTA TTCCTCCTTT 120

AAAATTTCGA TTGCTTTTAC ACTAGCATTG AATGCTATAG ATGCACTGTA TGCATGGTTG 180

CTATATTTTG TGCCTAAATT AATCAGTCCA ACTGTTTGCA TATTAGATGT TGGGTAAATG 240

TAGAAGTTAA TTTTATTAAT ATATTCGGGT TGTAGACTGG GCAAAGTATA CTTATGAGCT 300

TTATTGTGTA GAAAGTCACT AAGCATACTA TAAAGCATTA ACATGCGTGA ATTAGCrTCA 360

AAGTCTTTGG CGTTTAACAC TATTGCAATA ATATATATTT GAAAATTTAT ACTAAATTCC 420

AAAGCATTyT CATAAAATAC ACCkGCTyTA kAATTATGAT CAAATAGATT TTCTGTACCA 480

GCAAATTTCA ATGCTATTAT ATTTGAGCTA GCAGCTGTGA TTTTTGAAAG ATATGGATGA 540

TTGTAGGTAT TTATGATATC GCACTCAAAA TTATTTTCAG TTGCATACGC CTTAAACCCT 600

TTAAATATTT TAGTTAAATG ATTTAATACC ATATCTAAAG TGAAAATCAT TCAAGTGTTA 660

CCTTATAAGT AATCTCTGAT AACATTTTGG CTGTATCAAC AAGTGGaATT GCTGCAGTGT 720

TACTACCCCT TTTAAACTTA CTTTTGA 747

(2) INFORMATION FOR SEQ ID NO: 120:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 744 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACACTTAATT CAAAAGTACT AAGCTTTAAC CCGGAAATCT TAAGAAGATT TGAGAATTGT 60

AAATTTTAAC CTAAAAAGCA GAACCTCATA AAAGTTTGAC TTTTACCCAT AACAGTATAT 120

```
AATATTAATA TGTTTTTTTT CAAATTTTTT TCAAAACATA AACCTGCTAG GAAAAAAAT      180

TATCATAAAA TCAATCCGGA TGAATTCATT CTAATTAGCG AACATCTTAT CAATTCTTAC      240

AGCATTACTC ACCAATTACT TGGGATTATC ATGGCCTCTG GAATTCCATT AACTCATATA      300

AAAAAATCAA AACATCAAAA CTCCTTACAA TTTCAAATCT GATATATTTT CTTATACGTT      360

GAACAACGGT TTGCAAATTC AAACACATTC TCTAATTTGC TCTAACAAAA TTTCTAGGTG      420

TATTGAAAGT TTAAACAAAA ACAGATTACT ATCTATTGGT GCAGACAAAA TTAATTATGT      480

AGCAAAAAAT ATTTTTGATT TTAGAATTAC TACTAAACAA CTAAAAATTA TTCATTCTTT      540

GATTGCTAGG TCAAAAGAAA CACTACATGA AATCAGATAT AACTCTCATT CACAAAACTT      600

CTTTTTAGTT AAAACACCCT GTATTTTAAA TCTGTACCAA AAGCTCAAAT ATATCAAGTC      660

ATTCGGCACC TCTAAAGCTC AATCAAAATA ATCTAAATTA TTATCGAAAC AGCTCCAATG      720

AGCTTACATC TACTATTACA AATT                                           744
```

(2) INFORMATION FOR SEQ ID NO: 121:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 721 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```
AGTTTGTnTA TTCCTAGTAA CAATAACATT TCAGAATAAA GTTTTGTnAC CAAAAGTTtT       60

CTTCAGCcTC AACTTGTGTT TGTAAGTTTT TTTGTTCGCT CACCTCGATT TACCTTATGT      120

TTTTAACTTT GTTTAATATG TACTTGCAAA ATAGTTTTTC TAGTAGCAAG TAACCCTCCT      180

AAAACAAAAT CAATGTATGA ATGAGCAATA TCAGTTGAAT CTTTATCCAC TTGTTCATTT      240

GGTGTAGGTA ACATATACTT GCTAGGTTTA AACTTAATAA GCTCTGGGTT TAATGGGTAA      300

ATAAGTATTT GATGTTTTAG CAAGTTTGAA GTTTCAATGT AGACATCTTC TCTATTATTA      360

ATAGCCyTGA TAGTTTGAAT CAAAACATCC TCCCATTTTT CGCAGCTACT TGCTGCACCC      420

TGTGCTGCTG CGTATGGCTT TACGAGTTTG AGCGAaGTTG TAGGgTCAAC TATTACCATC      480

ATAGGTGTAG AAAATtCGTC TCCTAGCTCT AACTTtGAAA GTCCCGCCTC AATTTTTtCA      540

AATATTTTAT CCATTTTATC TTTATCACCA CTAGCAACTT CTTCTTTTAC TTGATGTGGC      600

ATATTAAGAA GTCCATACAT ATTGGGAAGT AGACGTTTTT GATTTTTTCC ATCTTTTTGA      660

ATTGAAACAG TGCCTGTTAG TACAAAGTGA TTAATAAGTT TAATAATCTC GCTACTTGCA      720
```

(2) INFORMATION FOR SEQ ID NO: 122:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 720 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```
CAATTTCAGC TCTTAAATTT TCTATTTTAG TTCGCATACC AGTAAGTTCA ACACTAGAAT        60

ATTGCTTAAA TGCACGTATA AATCCTAATT TTAAATTAGC ACACTCTATA TCTAATTCAC       120

TTATAACTTT CCTAGCGTTA ACTTCTGATC TAAAGGTTTG CGATAAAAGG TGTTCTAAAG       180

TATCTTCACT AATTGTTACT CTAGCGTCCT GGTTAACAAT ACTTTCTCCA CTTTCCCACT       240

TTTGTCTCAT TCTCCACACA TTTACTTTAG AAACTCCTAA TTTTTTCGCT ATTTCTCTAT       300

CATTTAACGA TCCTTCTCTA AAATACACAA CATAATCATC AAAAGGCCTT TTAACTTTTT       360

TCAAAACAAT TTCTCCTAAA ATAACAAAAT TAACAAATTG TTACTCTAAG TAGTAAAGCA       420

ATTTATTAAT TGTTAACATT AACTGATAAC TTCTTGATAT TTAGCGGGGA ATATTTGTTG       480

GCCTTTATTG ATTTAGTTCG CTGCTATTTC TATAATTTTT GATTTAGAAA TAGTAGTTCA       540

TTAATTTATT GCATATTACT ATAAAATAAT TCTACTTTTT CGGAAAAATC TTTCATTTCA       600

TTCATAAGAT TTTTACTTGT GAAAAGTCTT TTATCATAAT AGTGTATACT CAAAAATAAA       660

ATATCTCTAA ATTCTTCAAT CGCATCtATT TGAAAGTCTA ATyCTAATAC TTTTCTCCTA       720
```

(2) INFORMATION FOR SEQ ID NO: 123:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 715 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```
TAATAAAAAA CTAAAGCTGT TCAACTGCAA TTGTTGCACT TGAAATTTTT TATACTAAAA        60

TAAAATACAA ATAATTATAT TAACAAATAT CGATTTTTAT AAAAAATAAG TAAAAGTAGT       120

CTAGTTTACC TGAGTATTTA AATACTTTTA ATTGAGGATG TTTTATTTTA AAAAGGAGTG       180

TAAAACTATG TCAAAAGCTG TTGACGAAGT ATATTGCTAT TCTTGTGGCA AGATTTAAAA       240

AAGATGCTGA GATTTGTATT TCTTGCGGAG TCAGAAATAA ACAAACCGAA AACTACAATA       300
```

```
AACTTATAGT ATTTTTACTA TGCTTACTTT TTGGTTATTT AGGAGTTCAC AGATTTTATG      360

TAGGTAAAAT AGGAACTGGT CTATTATACC TATTTACATT TGGATTTTTA TATGTTGGAG      420

TTTTAATCGA TCTTATTAGA ATAACAACAA ACAAGTTTAA ATGTAATTAA AAGGATTCTT      480

TAGTAAATTT TTTATTAGTC TTGTTAAAAT TATTTTTTAA TTTTTTAAGC ACATTTTGTG      540

TGAACTGCTA TTTCTATAAT CTTTGATTTA GAAATAGCAG TTCACTAGAT AATAATAAAG      600

CTAAAATTAA TATyTtAGTA TTTAATAATT CTTGAgAAAA nGTAAAATTG GTATATGTTT      660

ACTTGTTATA AAAAAATCTA TCTGGGTAGG ACTTTTAATG TTTAATAAAA TAGTG          715
```

(2) INFORMATION FOR SEQ ID NO: 124:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 715 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```
GGAGGATTTA ATATGGAATT ATTTGATGAA AATTATTATG CAAAAGCTGT GGCAAATATC       60

ATAGGAGAAG TTAAAGATCC TATTATGTAT AAATGGTTTT CGCCCGATCA AATTGAAGAT      120

GTTGATCTAC AAATGGGATA TCAAAAAACC GTAAAATGGG ACGCGTTTTT AAATGCTAAT      180

CCTACAACAA TTGCCAATGA GGTTAATACT ATCTCAACTA TTGGATTTAG TTCTGAAGTG      240

GTAAGACTTA ATTATTTGAA ATTACAGTAT AAATTCAGAC ATTTAAAGCA GACTTCTGAG      300

AAATTTTATA CTTCAGATTC ATATATTGGG GACATTAATA ATAATTTACT TCCTTTTGCT      360

CAAGCGTATA AGCTTGCAAG TAGTGAAATT ATTAAACTTA TTAATCACTT TGTATTAACC      420

GGGACTGTTT CGATTCAAAA AGATGGGAAA AATCAAAAAC GCCTGCTTCC AAATATGTAT      480

GGGCTGCTTA ATATGCCCGA GCAGATAAAA GAAGAGGTTG CTAGTGGTGA TAAAGATAAA      540

ATGGATAAAA TCTTTGAAAA GATTGAGGCT GGACTTTCAA AGTTAGAACT GGGCGACGAA      600

TTTTCCACCC CGATGGATGG TAATAGTTGA CCCAGCAACG TCACTTAAAC TAGTAAAACC      660

ATACGCnGCA GCACAGGGTG CAGCAAGTAG TTGTGAAAAA GGGAAGATGT TTTAA          715
```

(2) INFORMATION FOR SEQ ID NO: 125:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 714 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```
GTATAAAAAG CAAAAGAAAA ACATCTTCCT TCACAGAATA GTTGCCCAAA TCCAATAATA      60

ATTCATACTG GTTGAAAAAT TTCCAAGAAA ACGCAAATTA TTATTGGTGT TCATATTGTT     120

CAACATCTAG ACCAAACCGA AGTGGAGTGG CCTTTTTCTT ACTTCATTTA GTAAGTTTTC     180

AATAATTAAA CCAACAGGTA GTATTAAAAC AAAGTTTTAA TACTACCAAA GTTTTAATGG     240

CTCCTTCAAA ACAGCAGTTT TAACCGTTTC ATTCTCTCTT CTGCTAATAG TAACTGGTCA     300

TATTTAGTCA TTCCTCTCAA AACACCAATT GATGTAGCAA CAATTATCAA ATTACTAACA     360

TTAAAAAACT AAAAATATTA TAAAATATCC AAAAATAAAA ATATTCTTAT TAATTAAATA     420

ATTAATACTA ATTATTTAAT TATAGTATTA TTGCATTATA TTATAGTTAA GGAGAATATC     480

TATGAAATAC CATATAATCG TAAGTATATT TGTTTTTCTA TTTTTAAATG CTTGCAATCC     540

AGATTCTAAT ACCAATCAAA ATAATTCTAA AAAGGAATTA AAAACAGGAA GAATCCCTAA     600

TAAACAAATA AAAAATGCCC TACTTGgATG ATTTAAAAAA TTTAATAGAA ACAGCTAGTG     660

CAGGATAAAA AAATATGAAA AAAATTAGGA AGAAGAACCT TCAAACCAAT ATGG          714
```

(2) INFORMATION FOR SEQ ID NO: 126:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 708 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
GnATTAACTG GGAAAAATTT CTCAAGTGTA ATTTTATATT CTTTTATATA ATTTTCATTT      60

AAATCGAAAG TATCGTTCTA TGCTATCCCC TTGTTCAAGT CTTCACGTTC ATGAATGGGG     120

CCTAAAAAAT TATCATCACC GCCTATTAAT TCCAATAAGT GTTTTCATTA CCAAAATTAC     180

ATTTTTTGCA TATTTTTTAG TTTAAGTTTA TTAATTCTTT TTTTACTTTC GTTTTCTCTT     240

TTTTATTTTT TATTTTTATA AATCACTTTT ATTTAAAATA TATGTATACA TATATTTTTT     300

TTACTATCTC TTTTAATAAG CCCAGACAAA TAATTACAAA TATCACACAT TAAGCAACAC     360

ACGTGCTCTT GCAATTTTGA TTTTTTAAGC CAATCTCCAA AAAATTTTTA AAAAACTTAT     420

TATATTTATT GATTGCCCyT TAAGAAACTT TTTTTATTAT GCyTTTATTA TAACTTTGTA     480

AAyCTTtCAA TAGTTTAACT TAGATAGATC GGAAAATACC TTGnCTATTA GGGCTTTATT     540

ATAACTGTTA AATTTTGnCn TTTTTTGTTA AAATTTATAT TGCCAATGAT AAAAATACGC     600
```

CAATTTAAAT TAAACATTTT AATAATGTCC AAATCCTCCT TATATAAGGC ACATCATAAA   660

TCAATTTTAC TGAAAAAACA AAAAGCATAT CTAAGATTTC ACCCTATT   708

(2) INFORMATION FOR SEQ ID NO: 127:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 703 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GGCCAACATG AACTATAGCC TAAAAATCTA AAAGACTAAC TTGAATTTTC TAAAAATCGT   60

AAATTTTAAC TCAAAAATCT AAACCTGCAA AATTTTAGAT TTATTACAAA GAAGTCTATC   120

ATAAACTTCG TATAATCTTG TTTCAACTCT ATCTAATCTG GCTTTAAATT CATTACCAAA   180

GCAACTAAAT CTTTAGTTTC AAATTCAAAT ACCACTCTTT TATCTAAATT ATCTATTTTA   240

AAAACCTTTA GCAATATCTC AGTTCTTTTT TTCTACCTCA TTTTTTAGTT TAAAATTTTA   300

TTTTTTATTT TTTTTATTAA CTTATTTATG ATAAAAAATT TTATTATTTA GTAAATAATT   360

ATCATATCCT TTTATTAAAG AAGAAATATA ATCTTCTCCT TTTTTTTTAT TCTTTAATGC   420

CTTAAAATCA CCAAGCAAGG TGATAAAATC TTCCTTAGCT AATGAGTAAA GACTAGCTAT   480

AATAAAATTA TTTTCATTTT CTTTTTCTTT AAAAAATTCA TCTTCTTTAT CTAGTTTCAG   540

TATTTTATTA ACTTTTTCTT TATCAAACTT AAAATATTCT AAGTAAAGTA AATATTTAAA   600

GTTTTCGGGA TCATTTTTGG CTATCAGTAA AGAAGTATTT TTTGCAAGAT TTAAATATAA   660

AGGATTACTT AAAATTTCCT TTTCTTCGGG TTGAGGCATT GGG   703

(2) INFORMATION FOR SEQ ID NO: 128:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 699 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCGACTCAAA ACTTTACCCT TTAAATTGCT AACTTTAACT TGAAAATACT AAACTTTAAC   60

CCGAAATGAT AAAACTTTAA TTTTTGCAAT TTTATTCTCT TGTTTTTTTT AAAACGATTA   120

GAATAATCGT TGAKCAGGTT TATTGATTAT CAATAAACCT GATCTATAAT ATTATAAGCG   180

GTTTTTGCAA GTTTAATAGG AGCTATAATA TCCATGAACA AATTATTGAT ATTCATTATT   240

TTATTAGTCT TTTCATGTAA TTTAAGTAAT TCTGATCAAA ATAATCCACT AAACATGTCA   300

AATAAAGAAA AAATAAGCGA ATATCAAATA AATGAGTCGT CAAACAAATA TTCAATTTTC   360

AAACGAAATT CAAGCGTTAA AAGATACACG TTCAACCATT ATTACTAACC AAAATGATAA   420

TATTAATTCT ACTATTAACT ACCCACCTTA TATTCAAACT ATCTTAAAAA TAGAAAAACA   480

AGTTGACGGA AATATTATTA TTAATGGGAT GACTAAAGAA AGTGGCACAG AAACTAAAAA   540

GCTTTTAGAA ATTCCAAATG GGAATATTTC TCGACTTAAA GATGCAATTC AATATGGAGG   600

AAGTTTTAGG GCTAAAGATG TTAGAGAAAA TCAAACCCAA AAAGAAAACA ACAAAGACTC   660

GCATATTCAT GTCGaCAtTT TAAAGATACA TACTTTAAT   699

(2) INFORMATION FOR SEQ ID NO: 129:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 695 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GTGGCAAATA ATAATGTATT GTAAAATTTG ATTTTTTAAA ATGGTACATT ATAATATTGA   60

TAAAGAGTAT TATCAATTAA CACTTAATTT TTGCTTTTTC ATAAATTAGA ACTTATTTGA   120

ATTTTTTAAC AAGAGAATTT AAATAGGTTC TTTTATTTTA ACAAATACAA ATTGATTTTA   180

ATTCTAAATT AGAATATATT CAATTATTGA AAAGCTTATT TAAATTATTT TAATAAGCAA   240

ATTTGATTAA ACCCTAACTT TATTAAAATA ATTTATGTAA AAAGTTGTCA AAAATAGTTT   300

TTGTTATACA TATATATATG TATGTAAATA GCTAAAAAAG TTTATTGCTA TCAAAACAAT   360

CCAATCAAGT TGGGTTTAGC TAAGTTCTTA GATAAGAGAA TTTAAATAAA CCCAACTATT   420

TTTTTGTAAA ATTTTTTGTA AAAAAGCCTG ACAAAAATAG TTTTTGCTAT ATACTTATAT   480

TTTTTACTAT AAAAGGAGTA AAAAGATGGA AAATCTTTCA AACAATAATA ATCCACAAGA   540

AAATATTCAA GGAGAGCTCA AAATGATAAG TATTAATCAA CAAAGTTTTA CTGGTTGTGA   600

AATATTTGAG GAAAAATCTT CTCCCATTAA AGAAAAAGT AAATTAAGTA AGATAGGTAA   660

GAAATTACCA GGAATAAGTA GTCAAGAATG TTTTA   695

(2) INFORMATION FOR SEQ ID NO: 130:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 684 base pairs
        (B) TYPE: nucleic acid

    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CAAGCAAGGG TTAACAACTA CCTTAAAGAC AAATTTAATA AAAAAGGGAA TCTAAATTTA   60

GAGGAGTGTA ATAATAATAA TAATAATAAA GAAGAAGAAG AAGAAGACAT AAGAAATAAT   120

AAAATAGAAA AATGTCAAAT AAAAAAATAT TTCAACAAAT GTAACTTTTT ATCCGAAGAA   180

GCTAAGTCCA TTTTAGAATT AAACATTAGT AAGAATAAAA CAATTGAAAT AATAAAAATA   240

ATAAAAAAAA TTGAAACCGA CTTAACAAAA AATAAAAACA AAGTTTGTTT TAAGAAAAAG   300

CAAAAAATGT TGAAAGAAAT ACTAAGCAAA ACTAAAAGC AATTAGAAAA AAAAGGATAT   360

GACACCAAAC AACTGAAACT CAAAATCGAA AACATATATA AAAGTTATAA AACCAAGCCC   420

CATTTTATTA TTGAAAATAA AAAATACAAA GACCTAGACA AAATAAGGCT TAAACTAGAA   480

AAATCAATTG AAATTAAAAA AGAAAGTATT ACAAAAAAAT ATATACATAT AAAAGTAAAT   540

ATTTTCAACA TACTAATAGA ACAATTGAAA AAAGrmTTGG rAATAAAAAC TTTAAAGCCA   600

ATTATAAAAA ATTATCTAAA TAGCnAAAAA ACCCTAGAAT ATGATAAAGT GTTCAATACC   660

TATTATTATG nACTATTAGA AACT   684

(2) INFORMATION FOR SEQ ID NO: 131:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 673 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GTATAAATTA TCTTTTAAAT TTATTACTAA ATCTCAAATT AGATATATAC TTTGTGTTTG   60

TGCATAAACC AACTCCAGCT TTAAACAGAT CACAAGCGCT AAAGAACTTA CTAATCTACT   120

TGCAACAAAC ACCAAAACTT TGAAATAAGA AATTCAGTCA ACCTTAATAG CAAATCAAGA   180

AAAACCAAAT CTAGATATTG ATAATTGACG TACAAAAAGA AATAGACAAC ATAATTTCAA   240

ATCTAAAAGA GTTTATTAAA ACTCTACAAA CCCTACATTA AAATCTGCTT AGCATAGCTA   300

AGTATGCTCA ACAACATCTT AAAAAATTCA ATTCCAAAAA TAAAATCTAA AAATTGCACT   360

ATTATTTAAA TATCAAAACT TAATTATTAG GAGGTAATAT TAATATGAAA AAAATTTTCA   420

CATTAATATT AATTTTTAGT TTAACGATGC AAATCTTTGC TTTAAATTTC ACTTCAAAAT   480

```
ATAAAATTCA GAAATATGCT GAAAGAGAAA AGGAGTTCAT TCAAAACCAG AAATTAGAAA      540

AAATTTTGAA AGACCCCGAA AAGACTAAAA AGGCTCTTTT GCAATACGAA AAAGAACAAT      600

TGATAGATCT ATGGATTCCA GTAATGTTAA ATTTATTTTT ACCTTTTGGA GTGGGGcTTT      660

TGTCCAGGAG ATT                                                        673
```

(2) INFORMATION FOR SEQ ID NO: 132:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 660 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```
CGAGTATTTT GACTCAAAAC TTTACCCTTT AAATTGCTAA CTTTAACTTG AAAATACTAA       60

ACTTTAACCC GAAATAATAA AACTTTAACT AGAATTTTTC AAAATGATAA AACTTTAACC      120

CGAAATGATA AAACTTTAAT TTTTGCAATT TTATTCTCTT GTTTTTTTTA AAACGATTAG      180

AATAATCGTT GAkCAGGTTT ATTGATTATC AATAAACCTG ATCTATAATA TTATAAGCGG      240

TTTTTGCAAG TTTAATAGGA GCTATAATAT CCATGAACAA ATTATTGATA TTCATTATTT      300

TATTAGTCTT TTCATGTAAT TTAAGTAATT CTGATCAAAA TAATCCACTA AACATGTCAA      360

ATAAAGAAAA AATAAGCGAA TATCAAATAA ATGAGTCGTC AAACAAATAT TCAATTTTCA      420

AACGAAATTC AAGCGTTAAA AGATACACGT TCAACCATTA TTACTAACCA AAATGATAAT      480

ATTAATTCTA CTATTAACTA CCCACCTTAT ATTCAAACTA TCTTAAAAAT AGAAAAACAA      540

GTTGACGGAA ATATTAATGG GATGACTAAA GAAAGTGGCA CAGAAACTAA AAAGCTTTTA      600

GAATTCTAA ATGGGrATAT TTCTCGATTT AAAGATGaAT TCAATATGGA GGTAGTTTTA       660
```

(2) INFORMATION FOR SEQ ID NO: 133:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 656 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```
AGCACTTTAA AGAAAAAAAA GAAGAAAGAT ACCAAAATAG AGTTGCCAAC TATTTCAACA       60

AAAATTCTGA TTCAAAAATG GGTAGTGTGC AATTGGGGGA GTGTAATAAT AATAATAATA      120

ATATAAAAGA AGAAAGAAAA ATTAACGAAA TAGAAAAGTA TCAAGTAATA AAATACTTCA      180
```

ACAAGTGTGA CTTTTCATGT AAAGAAATTC TTCCAGTTTT ATTAACATTA AATATTGATA   240

AAGAAAACAT AATTAAAATA ATAAAAATCC TAAAAATAAC CGAAATTAAC TCAAAAAATA   300

AAAATATACG CCCTACTAAA TCTTGTATTA AAAAAAAACA AGAAAAATTA AAGGGAATTC   360

TATGTAACAC TCAAAAAGAA TTAGAAGAAA ACGGGTACAA TCCCAAACAA TTAGAAATAA   420

ATTTTCAAAA AATATACGAA AATTACAAAT ATAAACCCCA TTTTATTATT GAAAATCATA   480

AATATAGCGA TTTAAACAAC ATAAAACGTA AATTGGAAAA GTCAtTGAAA GAAAAAAAGA   540

AATTCTCAAC AAGATTATGA aATTTAAAGA TAAACGTTTT CAATATCCTA TTGAACAACT   600

AAAAAAAGAA ACAATATTGA nTTCTAAAGC CCTTATAAAA GAATTTTGAA TACCAn   656

(2) INFORMATION FOR SEQ ID NO: 134:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 652 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

TGnAATTAAT GTATCAAGCG ACTCTTTGTA TCCAGTACTT TTACTGTAAA ATGTAGTCCT   60

AACAACAGGA ACTTCACCAT TTTTACCATA CACAAAAGTT GGAAATTGCC AAAAACCAAG   120

CTTTAAATTG TGATTTTTTA TAACATTTTG AATTACTTCT ACTATGACAT TGAAATCTTG   180

ATACTTATAT CCGTATCCTT TAAGACTTTT GTCAATACGT GGCAAGTTCA TTCTTAAAGT   240

ATCCATATCA TTTAAAAAGT CTATTTCTGC TTGAATATTA TTTTGTATTT CTTGATTATT   300

ATTGTTTGAA ACATTGTTCA TGTTTTCCTC CTTTATTTAG TAATAAATAA GTATATAGCA   360

AAAACTATTT TTGTCAGGCT TTTtACAAAA ATTTTTACAA AAAAGAAGTG GGACTtAACC   420

AAACTCTTTT CTTAAAGAAT CTCGTTAAGT CCCCACTATA TTATTATTTT TTGCAAATTA   480

CTAAATAAAG GTAGTCAAAC TGAAATATGT TCAAATAACT ACGCTGTTTG TAGTGTAGCC   540

CAATTTTTAA TTAAAATCAA TCAATCTTTT ACTAAGTTAT AAAAAGTATA TTAATTTAAC   600

AAAATTAATA ATTAAAATTT AATATTTTTT TAGAAAAGTA TTTAnCTTTA AA   652

(2) INFORMATION FOR SEQ ID NO: 135:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 649 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```
nAATTCGAGC TCGCGTACCC AGAAAGTTCA GTTAACAAAA TGTAGTCATG ACTACCTAGT        60

GTCACTTCAA TGTTGAAAAC ATAAGTTATT GTTTTGGGAT CTCTTAAGCT TATTACAGGC       120

ATACCTTTAT CTTCACTACT AATCACTGCT CTTGTTGTAG GTTCGCTTGT AAGCTCTAGC       180

TTGCCACTAT GTAACTGCGT ACCACCAATT GAAAAATAAA CTTCTCTTAA ATCATAAAAT       240

TGCATTTTTA GACCCCCTTT TAAGCACTTA AGCTGTTTTG ATAATCAAcT ATATCTTGAG       300

TAGTAATTAC TAAAGCAACA GCATTAATGC TAAAGTTATA AGTAATAkTC ACGCyAAGTT       360

CTAATTTAAG TTGyGGkGTA GGAGAAAGAG TAAGAyTTAA ATTTTTrTAC TCwATwATCA       420

GTCCTCTATC CACAAACCTT TTCAGTAAAC ATTCAATTGC TGAAGTATAT GCATTGTCTC       480

TAGCTCCACT AAGCTGCAGT GCAGATAATT TGCTATTTTG CCTATTGTTT TTGTTCCAAA       540

TTyTAATAAG CTCAATAATC GCTTCGTTTT TTATATAGTG GTATGTAAAT TGTTCGTCTA       600

TTGyACyTCC AGCTAGGTCA ACACCTTCTT TAAAGGCAGG TAAACCATC                   649
```

(2) INFORMATION FOR SEQ ID NO: 136:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 644 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
TAAGCAAAAG GnCCTAATGT TCAnGATAAT CCACAATTAG GGTTAGAATC AGAAATTCCA        60

GTTGCTCCTA GATCTAAACG TCAAGCAAGA CAGGCTGAAG AAGCACAAGC AAAAGATCCT       120

TATTTAGATT CAGTTAAAGA ACTTGACGAT GTTCTTTTAA AATTTAAAAA ATATTCAAAA       180

TCAATGAGTT CGATTGAAAA TAAGGTTTTT AGTAGTTCGG GtGGTTGTTT TAAATCAAAG       240

AATGmGCGAG TTAATGCTTA TTCTTTTACA TrTTCAAGCT TTGCAGACAA AATAGAAGAA       300

TACCTTTATG ATCCAGCAAA TAGTTTTCCA TATAAGCGTG GGGTTAAACT TGTTCCAAAA       360

GAGAAyTCTA TATATGTTGA AGTTGGTGCT GATACTGATA TGTATGGGAT ATGTGTAGAT       420

GTATGTGAGT TTAGTAGTAC TGCGTATGTA TTACCAATTA CGAATAACTT TGAAGGGTwT       480

CTTGTTACAA GAAATCCGAG TATAAAAATG GGaGAAATAT kGGaTATAAA TAACAATGGG       540

GTTATaTCAA GGCTGGTGGT GGGCCmCCAA cCGyAATTAa TGCATATGCC CTCTCTGaTT       600

CATTACAATC AATTTTGGCA CCCGAAGATG AAGATCAAGA TCAG                       644
```

(2) INFORMATION FOR SEQ ID NO: 137:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 636 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```
AAAAAGTAAT GAATCATGCA TGCAGATTAC TTATTCTTAC CATAACAATA TTTGAAATCA        60

ATTTAATATT AGAAAATTAT TCTCAAAAAA CTCTACTCAA ATTTTATAAC GAAAATCTCA       120

AAAACCGAAA TCTAACTCCT AGTGTTATAT CAACAATAGA AAAATACTTA AACCAATTAG       180

AAAAAGAAAT AAACGTCATA GTCGAATTCT ATTTTAAAGA CAATCAATCC ATAATTTATT       240

ATAAACTTAA TTACACCCTA GAAAAAGTTT GCTTAAAACT ACAAGAATAC TACAAATTAT       300

TCTACAAAAA ATTAAAACAA TTTTTACAAA AAAACACTAC TACTACTTAA TTGTAAAAAA       360

TTATATCTTT GCAAATTAAG CAAATTTAGA AATATAAATT GCAAGATAT  ATATTTTTAT       420

ATGATAAATA ATAAAAATTA CTAGGAATAC TAACTTGGAA AAACTTTTGA AAAAAATAAT       480

AAAAATGAAT TACAAAAATA AGCTATCTTC TCACTTAATA ATTCTTATTT ACACACTAGG       540

CGACACTGAA CTAAATTTAA ATATTGAGTA CTATAGTAGG GGCTTTATAC ACCACGTGTT       600

TAATTCTAAC ATACATAAAT ATTGCAATAC TACTGA                                636
```

(2) INFORMATION FOR SEQ ID NO: 138:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 632 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```
CCAATAACAT GACTTTAAAG GTTGCTTATT GACAATATGT TATTTTTCAA CTTTGTTGCT        60

TGAGAACTTT TTTTTTCAAT TTGCTTGTAA AGTTCCGTTA AATGAGATTC AAGCTTAGCA       120

ATATCTGTTT TTATAGAATC CTTATCATCT TGATAATCTA ATAAAAGTTG GTTTAACATG       180

TCTGATACGA TTGATTTCAT GGATAATAAT TTTTCAAACG AATTTTTAAG CTTCTCTAAA       240

TTTGAAATTT CTAGTTTATC TAAAGCATCC TTTTTAGGAT ATAAGTGATT AATCGCTGTA       300

TCAAAAGTTC TTCCAAGGTT GCAAAAAGTG CCAAATAGGA GGGTTTTTTG TTTTGATTGA       360
```

ATTAAAATCT TTGAAAGATT CGCTAACTTA TTGGTATTAA TAGGATTTAA AGTAGCATAA   420

GTGAATTTTC TATAGTTTTT AGATCTATCG GTATTATCTG CTACCGTTTC ATATGATGCT   480

ACCCAATAAA TTTCTTTGAA AATTGATATT CCATATTGGT TTGAAGGTTC TTCTTCTAAT   540

TTTTTTTCAT ATTTTTTTCT ATCCTCGTTA GCTGTTTCTA TTAAATTTTT TAAATCATCA   600

AGTAGCTTAT TTTTTATTTG TTTATTAGGG AT   632

(2) INFORMATION FOR SEQ ID NO: 139:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 628 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

GACTTCTTTA ATAGATCAAA AAGCTCACTT CCATCACCCC CAAGAACACT ATTAACAGCG   60

GGGATCCTCT AGAGTCGACC TGCAGGCATG CAAGCTTGGC ACTGGCCGTC GTTTTACAAC   120

GTCGTGACTG GGAAAACCCT GGCGTTACCC AACTTAtCGC CTTGCAGCAC ATCCCCCTTT   180

CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAn   240

CTGAATGGCG AATGGCGCCT GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA   300

CACCGCATAT GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGCCC   360

CGACACCCGC CAACACCCGC TGACGCGCCC TGACGGGCTT GTCTGCTCCC GGCATCCGCT   420

TACAGACAAG CTGTGACCGT CTCCGGGAGC TGCATGTGTC AGAGGTTTTC ACCGTCATCA   480

CCGAAACGCG CGAGAcGAAA GGGGCCTCGT GgATACGCCT AwTTTTATAG GkTAATGTCA   540

TGaTAAtAAT GGtTTCTTAg AACGTcAGGg GGCAyTTTTC GGGGGAAAAG TGCGGGGGAA   600

CCCTAATTGG TTAATTTTTC CAAAATAC   628

(2) INFORMATION FOR SEQ ID NO: 140:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 621 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

ATACCGCTAA ACTCATCTAT ATCGGAACAC ACTCCATATA AATCGTCTCC ACCACCAGCC   60

TCAACTTCTA GTTCGGTTGT TCCATCTCCA AAACTAAGCT TAACACCCCG TTTATACGGA   120

```
TACCCTTTAG CnGGtAATTC TCTATTTTGT CTTTACTGCT AGTGCAAACC CCACCAGAAT     180

TGGAAAAAAT TAGATTTtGG TCTCTAAAAT CAATAGAATT GCTAAGCAAT CCTGAGTCTT     240

GTTGGGGATT TTTCATTAAT GCTTGAATTT CTGCAACTTT CTTATCAAAT TCTTGTTTAA     300

TTTTTGTTAT ATCACTCATT TAAAAACTCC TTTAGGCAAT ACTTGTTCTT TTATGTCTTT     360

TTAGATTTTC ATAAAATTGA ATTCGTCTTT GCTTGTATGT ATTACTTATC GCTTGTACAA     420

ATTCTGTGAA ATTAATAGGT ACAAAATTAG AATCAAGCAA ACTTGCTCTT TCTTCTGATT     480

TAATAGCAAT ATTCCCCTTA ATAGAGTCAA CAGAAGAAGA ACTGCTACTC GCATTTTTTC     540

TTAATTTAAT ATTCACTTTT GCTAAAGAAA CAAGTTGCTC TAATATCTCT CCATCGATAT     600

GACTTATGTC TGATACTTTG G                                               621
```

(2) INFORMATION FOR SEQ ID NO: 141:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 608 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```
TCCAACTAAT AGTTATTGAT TTGTTCTTGT AGTCAGACGA TAAGCGTTGG TCCGTATGCA     60

AAATTtCTTC CATGTGAAAA ATCTGATGGT GCTCCAAGCA GTTGTTTTGG AACGGGTGTT     120

TTTTGAATAC TTGAAGAAGA CATTATCAAA AGATCATCAT TTCTAGATAG AGTGGCTGAT     180

GATATGCTAT TTGTAAGGCG TGATTTAATT TTACTAAAAA GGTTAGAAAT ATTAGTAGAA     240

TCGTTGTTAA TTAATTTGTC CGTTATTTTA GCATAAATTG TTTCTACAAA ATCTGTATTG     300

GCTGCAAGTT CTTCGGCAAT TGTAGACTTA ATTATCTGCT TAAAATAGTC TAATCCTTCT     360

CCTTTAAATA TTTTGTCTTT AGAAGCATCT AAAAAGTTTT TAAAGGTGAT AGCATTACTG     420

CTTGCAGCTC CATCATCAAG CAGTAAAAGA TCAGTATTGT TAACGGTCGT AACCTTATTT     480

AAATCTTTTA TTTGAACCGT TTCTTCTTCA TCAATTAGTA ATTTTTCTTG ATCATCAGCC     540

ATAAAACCTC CTTAGTTGTT AAAAGTTATA ATATTGTTAC CATCTGTATT ATTAATTTTG     600

AGAACTCT                                                             608
```

(2) INFORMATION FOR SEQ ID NO: 142:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 591 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```
CTCCAATAGC GCTAAAAGAA TTAAATATAC TTGCTACTGA TGCTAGTTTA TTTATATCTT      60

GAATAATATT TGCGAATTCC TTTAATTCAT GAGGATCCAG GGGGCTTAAA ACAGTATAAG     120

TGTGTCTTCT ATATCTTATA GATCTTTCGG TATTGTCAGA TATATCTTCA GTCCCTGGCC     180

CCCAATTCAA TCCCCTAAAA GACGTCATCC CGTAATGGTC TTCAGGTTCT TTTTCCATAC     240

TTTTTACATA TTTTTCTTTA AAATTGTAGG CCGATTCTAT TTGCTTTTTT AAATCATTAG     300

ATAGCGTATT TTTTAGTTGT TGTTTTCTTA GTTCTTCCTT CTCTTCTTCT TGTTGTTTTT     360

TCTTAAGCTC TTCTTCTTGT TGTTTTTTCT TAAGCTCTTC TTCTTGTTGT TTTTTCTTAA     420

GCTCTTCTTC TTGTTGTTTT TTCTTAAGCT CTTCTTCTTG TTGTTTTTTC TTAAGCTCTT     480

CTTCTTGTTG TTTTTTCTTA AGCTCTTCTT CTTGTTGTTT TTTCTTAAGC TCTTCTTCTT     540

GTTGTTTTTT CTTAAGCTCT TCTTCTTGTT GTTTTTTCTT AAGCTCTTCT T             591
```

(2) INFORMATION FOR SEQ ID NO: 143:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 586 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```
GTGTTAGTGT CCCCATGTGA ATGGGTGCAC TAAAAAATTA AAAAAATAAA TTTAATATAG      60

GAGGATTAAT TAATGCTTAT TAATAAAATA AAACAAGATA ATAGAACTTT AAGACCGGAG     120

ATACAAAAAT GGGGTTGTTa CTTTTTGTGT CTGCATTATT ATACAAGTCT ATTTAAGCAA     180

CGTGAATTTA ATGCATATGA AATAAATACA GCGTATTATA GATTTATAGG ACTTGGTTAT     240

ATCAAGAGCA ATTGTTTTAT TATAAATCCA TGTATGATAC TTAATTATTA CGGAATTAGA     300

AGTAGCGTGA GATATGAAAC TGCAAATTAT TTGGGTGCAG CAAATGAATT TGAAATAAGT     360

GAAGTTAAAA TCGATAAGGk TAATGGATAT CACTTTATAT CAACAAAAAA TAAAGAAATA     420

TTATATGATT CACTTGaTTT AAAGCCACGT GGAAAAATAT TTAAAGTAAC TTCmAAACGT     480

wTwTTTAAAC tGrAATAGTT TaCTAAgTTT AAGGCACTTT TaGCACATTC ATAgCTgAAT     540

TTaTTAGCAG rAGrTAGGcC GTAGGATATA ACCAATTTCA TTGGTT                    586
```

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 585 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
GTGTTTTTTA GCAATTTATT TTCAACTCTT TTTATGTTTT TGATTATTTT AATCATAGTA       60

TCTTTATCAA CATTTAATGT TAATAAAAAT GGAAGAATTT CTTTACATAA GAAGTTACTT      120

TTGTTGAAGT ACTTTATTAC TTGATATTTT TCTATTTCGT TAATCTTTCT TTCTTCTTTT      180

ATATTATTTT TATTACTTAA ACACTCCACT GAATTTACAC TACTATTTTT GGAAACATTG      240

TCTTTAAAAT GkTTATTAAC TCTAGATTTA AATCTAGAGT TTTTTyGyTC TTTAAAGTAC      300

TTGTTGATTT TCTGGTAACA yTCTTTTTTA GGATACTTTA GCTTATAGTA AATTTCAGTT      360

CCACAATTTA CACCCATrTG TTGGTAGTAA TTAGTTGTrA CTTTTAATAC TTTTTCTAAT      420

TtGTAAAGAT AATTTtGCAT tGTTCTtAGw GTAGTGGGAG CTAGACCAkT CcTTTTtAGA      480

TTTtCryTAw AGyArTAGAG TATGTTTTGT TGCGTGTATT TCTTATCTTT TTTGGTTAGG      540

TAATCTAGCG TTGAAGTAAG AGAGATTAAT TTGTGTTGGT GTTTG                      585
```

(2) INFORMATION FOR SEQ ID NO: 145:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 575 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```
GGGAGATTTA ATATGGAATT ATTTGATGAA AATTATTATG CAAAAGCTGT GGCAAATATC       60

ATAGGAGAAG TTAAAGATCC TATTATGTAT AAATGGTTTT CGCCCGATCA AATTGAAGAT      120

GTTGATCTAC AAATGGGATA TCAAAAAACC GTAAATGGG ACGCGTTTTT AAATGCTAAT       180

CCTACAACAA TTGCCAATGA GGTTAATACT ATCTCAACTA TTGGATTTAG TTCTGAAGTG      240

GTAAGACTTA ATTATTTGAA ATTACAGTAT AAATTCAGAC ATTTAAAGCA GACTTCTGAG      300

AAATTTTATA CTTCAGATTC ATATATTGGG GACATTAATA ATAATTTACT tCCTTTkGCT      360

CAAGCGTATA AGCTTGCAAG TAGTGAAATT ATTAAACTTA TTAATCACTT TGTATTAACC      420

GGGACTGTTT CGATTCAAAA AGATGGGAAA AATCAAAAAC GCCTGCTTCC AAATATGTAG      480
```

```
GGCTGCTTAA TAGCCCGAGC AGATAAAAGA AGAGGTTGCT AGTGGTGATA AAGATAAAnG    540

GGTAAAATCT TGAAAAGATG AGGCGGACTT CAAGT    575
```

(2) INFORMATION FOR SEQ ID NO: 146:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 571 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```
TTGGTTCCCA nCnTATTTCG TTGAAATTGT GATACTTATA GCCATAACCT TTAAGATTTT    60

TATCAATCCC CGGCAAGTTC ATCCTTAGGG TTTTCATATC TCTTAAAAAG TCAATTTCTG    120

CTTGATTAAT TTCTTGTGGA TTATTGTTTT TGCGGTTTTT CATTTTTTTA CTCCGTAAGT    180

TATAATTTTC TTATATATAA ATATATAGCA AAAACTATTT TTGTCAACTT TTTTTAATAA    240

AAATTTTTGT TAAAAGACTT AGGGCTTTGC TAAATTCTCT TTTAAAAGAA CTTAGTAAAG    300

CCCTAATATT TTTACGATCC AATATTCAAG TAGGAAATAA TGAAAAATTA TTTCCTACAA    360

AACTATATTT AGTTTAGTTC AACCTTAAAT TAAAATCAAT TAATATTATT ACACTGCGGT    420

CTATAAAAAT ACAAAAATAT AAAGCTTTTA TAAAATCTTA TTTTAAAAGA ACTTATAAAA    480

ACCTATTCTC TAAATTATTT ACAAAATTCT AAAATTAGAT TTTTAGTTCT TCATATTTCC    540

TTAAAAGTTT TTTAAGAAAA TCTTTTTGAT T    571
```

(2) INFORMATION FOR SEQ ID NO: 147:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 555 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```
AAGCGTATAA GCTTGCAAGT AGTGAAATTA TTAAACTTAT TAATCACTTT GTATTAACCG    60

GGACTGTTTC GATTCAAAAA GATGGGAAAA ATCAAAAACG CCTGCTTCCA AATATGTATG    120

GGCTGCTTAA TATGCCCGAG CAGATAAAAG AAGAGGTTGC TAGTGGTGAT AAAGATAAAA    180

TGGATAAAAT CTTTGAAAAG ATTGAGGCTG GACTTTCAAA GTTAGAACTG GGCGACGAAT    240

TTTCCACCCC GATGATGGTA ATAGTTGACC CAGCAACGTC ACTTAAACTA GTAAAACCAT    300

ACGCAGCAGC ACAGGGTGCA GCAAGTAGTT GTGAAAAATG GGAAGATGTT TTAATTCAAA    360
```

1110

```
CTATTAAGGC TATTAATAAT AGAGAAGATG TTTACATTGA AACTTCAAAC TTGCTGAAAC      420

ATAAAATACT CATTTATCCA CTAAATTCTG AACTTATTAA ATTTAAACCT AGCAAGTATA      480

TGCTACCTAC ACCGAATGAA CAAGTTGATA AAGACTCAAC CGATGTAGCT CTTCTACATT      540

GATTTTGTTT TGGGC                                                      555
```

(2) INFORMATION FOR SEQ ID NO: 148:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 549 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```
GTTTCTTCTT GGAGAATTTT GATTTGAAGA TTTTGAATTT TGAGATTCAT TTTCAAGATT       60

TTGGTTATTT TCTGATGGAT TTTTTGTTGA ATTTCCTGTT AAATTTTCTG AATTGGTGTG      120

ATTGCTTGTG TTTTTTAGAT TTCTAGAATT GTTGCTTCGT TTTGTTTTTT TTAGACTTTT      180

AGAAGTGGTA GGATTTTTTG GTTCGTTTGG GTTAACATTG CCAAAAGGTG CACATGATAT      240

GCAAATTGAA GTTAATATTG CTGTAATAAC GTTAAGTTTA ATAATATTTA ATTTAAAGTT      300

TTTCAAAATA TTCTCCTTAT AAATTTGAAT TAATATTTAT TAATTTTAGT TCAAATATAT      360

AATATTACAA TTTAATATCA ATATCAAATA AGTTTAATAT TATTGATATT GAAAATTAAT      420

TTCATGAGTT TTAGCGGGAT TAGATGCATG AATTTAAAAA TAAAAGTAAT CTCCCTTTTA      480

AAATATGAAG TGnAACAATT GTTGGATTAA GGGGTTAATC CAGGAnCAGA GGGAATTAGA      540

AATATAACG                                                            549
```

(2) INFORMATION FOR SEQ ID NO: 149:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 544 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
TTTTGTAATT TTCATATTCA TTAATTAAAT GATAAGACTT CTTTTTTTAA TGaAAAATAA       60

TATTTCAAAA ATAAAATAAG CTCTTTTAGT ATCTTCTTTA CAAAATTCGT AAAACCCTTT      120

GTTTTTTATT AAAATCCTAA TAGACATTTT TCTATTATTT ACTTCAGGCA AATTTTCTTT      180
```

1111

TTTTTACGTT TGATAAATTC TCTTTTAACT GTCTTTGTAT TCCTCTAAAG CCCTATTTTT   240

TAATTTTATC TATATAAACA GGCCTCCTCT AAAACCCTTT TTCCGTAAAC TTTTTTTGCT   300

ATACTTTGTA TTAATAAATT TCCTAAAAGG AATTTTAAAA TTTTCTTTTA TTAAATCTTT   360

AAATACACTT TGATCTTCTT TTATACAAAG GGGAAATACA TGGCTTGATT CACTGCATCT   420

ATTTGAAACA AAACATCTCT ATAAAATTCT AGAGGTAAAA GAATGAAAAA AATTATTTGT   480

CGATAAAAAT CCTGTTGTAA TAAGGGTTAT ATTATTCTCn ATTTCCnAAA TATATTTTTT   540

TATA   544

(2)   INFORMATION FOR SEQ ID NO: 150:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 533 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

GAGACTTTGA AGCTATCTCG TCAGGGGTAG TGGAGTCAAT CTTGAAATAC CACCCTTGTT   60

TAATTAGGTT TCTAACTTAT AGAAATATGA GGAGAGTGCC AGGTGGGTAG TTTGACTGGG   120

GCGGTCGCCT CCTAAAGAGT AACGGAGGTG CGCAAAGGTT ACCTTAGAGT GGTTGGAAAT   180

CACTCTGTAA GTGTAAAGGC ATAAGGTAGC TTAACTGTAA GACTGACAAG TCGAACAGAT   240

ACGAAAGTAG GTCTTAGTGA TCTGGCGGTG GCAAGTGGAA GCGCCGTCAC TTAACGAATA   300

AAAGGTACTC CGGGGATAAC AGGCTTATCC TTCCCAAGAG TTCACATCGA CGGAAGGgTT   360

TGGCACcTCG ATGTCGGCTC ATCGCATCCT AGGGcTGGAG CAGgTCCTAA GGGTATGGCT   420

GTTCGCCATT TAAAGCGGTA CCGAGCTGGG TTCAGAACGT CGTGAGACAG TTTGGTCCCT   480

ATCTGCCACA AGCGTTGGAT ATTGAGAGGA GCTATnTTAG TACGAGAGGA CCG   533

(2)   INFORMATION FOR SEQ ID NO: 151:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 521 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

TGGTTTTGAA GCTTTTTTAG TAGGCTTAGA AGAAATTTTT AGTGAATTTT TAAGAATTTT   60

ATTTTCATTT AGCACATTTT GATAATCTTG AAATAGTTTG AGCATAAAAT CCATGTTGAA   120

ATTATTTAAA TTAAAATAAT TATTAGTGTT CATAAAATCC TCTCCTTGAA GGTGTTACTT   180

TTAAATTAAG TAAAAGTAAT AAAAATAGAT AAAAATAGTA ATTTATATTG TACCAAAAAC   240

GAAAAATTTT AGTCAAATTT TGTGAGTTCT CATTGCATGA GAAATTTGGG TTGTAGGGAG   300

GCTGTTATAA ATAGAATGGG CATTTTCTGA GGGTGTCGGC TAAGAAAGAC TACATACTTT   360

AGCTAATATA TAGCAAAGAC TTTGAAATTT AATTTGTATG TGTTTTATAG TCTTTTGTAA   420

TGAGTAGTGC ATTTGCAATG GAGAGATTTT GGGGAGTTGT TTAAAATTAC ATTTGCGTTT   480

TGTTAAAATG TAACAGCTGA ATGTAACAAA ATTATATATT T   521

(2) INFORMATION FOR SEQ ID NO: 152:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 501 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

GTTCTCAAAT TTTTATAAAT CTTGTTAGG AATTTTCTTT TTTTCTTTCA ATTGACTTTT   60

CTAATTTACG CTTTATGTAA CTTAGaTCGC TATATTTATG ATTTTCAATA ATAAAGTGGG   120

GTTTATATTT GTAATTTTCG TATATTTTTT GAAAATTTGT TTCTAATTGT TCTGAATTGT   180

ATCCACTTTT TTCTAATTCT TTTTGAGTGT TGCATAGAAT TTTCTTTAAT TTTTCTTGTT   240

TTTCTTTACT GCAAGATTTA GGAAAGTAAA TATTTTTATT TTTTGCTTTA ATATCAGTTC   300

TTTTTATGGT TTTAATTATT TTGATCATAG TATCTTaTCA ACATTTAAAT TTAATAAAAT   360

TGAAAGAATT tCTTTACATG AAAAGTTGCA TTtATtGAAA TAATTtATtA CTGATACTTT   420

CTATTcATTA AcCTTCTTCT cTTTATAtAt TTTATTACTA TTACAGGAnT CACACGTACA   480

CTACCCATTT TGAACCGAAT T   501

(2) INFORMATION FOR SEQ ID NO: 153:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 488 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GTTCCnCnTT ATCAAGGAAA TTAACGACAT CTTTCATTAT GGTTTCATTT GCAAATTTAA   60

1113

CAAAATTGTC TTTTTCTTTT TCTAATCTTT TTCTGAAGTT TTCAAATTCT GCTTGTTTTC   120

TTAAATACAA ATCTTTAAGA TTGGAGATTT CATTTTCAAG TTCAGCAATT TTTTTATCAG   180

AATTTACTAA ATTTAAGTTT TCTTTTTTTT GAGATTTTGT ATTTTTATTA TCTTGTTTGT   240

TGTTTTTTTC AGATTCGCTT TTAGTTTCTT TTTTTTCCAT TTTTCCTCCT kTGATAAAGC   300

ATTTTATCTT TAAAAAAAAT ATTTTACAAA TTTTnTTCTT TCytGAAATT TAAnAAAATG   360

GAGTCATTTT GnGGCATTTG TAAGATGTAG ATTTTTCTTA AGCTTTCAGT AAGAGTGTTA   420

TATGnATACA TAGGTTATTT AGTnAAAATG TTCGTGTGTA TTTTGTGTCA AAAGAAAAAA   480

TTTAAGTT   488

(2) INFORMATION FOR SEQ ID NO: 154:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 459 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

GGAGAGGCGG TTTGCGTATT GGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT   60

CGGTCGTTCG GCTGCGGCGA GCGGTATCAG CTCACTCAAA GGCGGTAATA CGGTTATCCA   120

CAGAATCAGG ATAACGCAGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC   180

GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCCTGAC GAGCATCACA   240

AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT   300

TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC   360

TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA TAGCTCACGC TGTAGTATCT   420

CAGTTCGGTG TAGTCGTTCG CTCCAAGCTG GGCTGTGTG   459

(2) INFORMATION FOR SEQ ID NO: 155:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 368 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GAACAAGAGT CGAAAGTAGG TGTTAGTGAT sTGGCGGTGG CAAGTGGAAG CGCCGTCACT   60

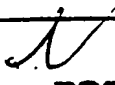TAACGAATAA AAGGTACTCC GGGGATAACA GGCTTATCCT TCCCAAGAGT TCACATCGAC   120

```
GGAAGGGTTT GGCACCTCGA TGTCGGCTCA TCGCATCCTA GGGCTGGAGC AGGTCCTAAG    180

GGTATGGCTG TTCGCCATTT AAAGCGGTAC GCrAGCTGGG TTCAGAACGT CGTGAGACAG    240

TTTGGTCCCT ATCTGCCACA AGCGTTGGAT ATTTGAGAGG AnCTATCTTT AGTACGAGAG    300

GACCGAGATG GACGAACCTC TAGTGTGCCA GTTATCCTGC CAAGGGTAAG TGCTGGGTAG    360

CTACnTTC                                                            368
```

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description
on page   8   . line   23

B. IDENTIFICATION OF DEPOSIT   Further deposits are identified on an additional sheet   —

Name of depositary institution

American Type Culture Collection

Address of depositary institution (*including postal code and country*)

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit August 8, 1997	Accession Number 202012

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)*   This information is continued on an additional sheet —

EUROPE

In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4)EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications. e.g. "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☑ This sheet was received with the international application	☐ This sheet was received by the International Bureau on
Authorized officer	Authorized officer

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later that at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:

    (a) any one nucleotide sequence of SEQ ID NOS:1-155; or

    (b) a nucleotide sequence complementary to any one of the nucleotide sequences in (a).

    (c) a nucleotide sequence at least 95% identical to any one of the nucleotide sequences of SEQ ID NOS:1-155; or,

    (d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences of SEQ ID NOS:1-155.

2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a) or (b) of claim 1.

3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) of claim 1.

4. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-155, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-155.

5. A method for making a recombinant vector comprising the step of inserting an isolated nucleic acid molecule of claim 1 into a vector.

6. A recombinant vector produced by the method of claim 5.

7. A host cell comprising the vector of claim 6.

8. A method of producing a polypeptide comprising:

    (a) growing the host cell of claim 7 such that the protein is expressed by the cell; and

    (b) recovering the expressed polypeptide.

9. An isolated polypeptide comprising a polypeptide selected from the group consisting of:

    (a) a polypeptide encoded by an ORF of any one sequence of SEQ ID NOS:1-155;

    (b) a polypeptide encoded by an ORF of any one sequence of SEQ ID NOS:1-155 except the N-terminal residue;

(c) a fragment of the polypeptide of (a) having biological activity; and

(d) an epitope-bearing fragment of the polypeptide of (a).

10. An isolated antibody specific for the polypeptide of claim 9.

11. A polypeptide produced according to the method of claim 8.

12. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.

13. An isolated polypeptide antigen comprising an amino acid sequence of an *B. burgdorferi* epitope shown in Table 4.

14. An isolated nucleic acid molecule comprising a polynucleotide with a nucleotide sequence encoding a polypeptide of claim 9.

15. A host cell which produces an antibody of claim 10.

16. A vaccine, comprising:

(1) one or more *B. burgdorferi* polypeptides selected from the group consisting of a polypeptide of claim 9; and

(2) a pharmaceutically acceptable diluent, carrier, or excipient;

wherein said polypeptide is present, in an amount effective to elicit protective antibodies in an animal to a member of the *Borrelia* genus.

17. A method of preventing or attenuating an infection caused by a member of the *Borrelia* genus in an animal, comprising administering to said animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.

18. A method of detecting *Borrelia* nucleic acids in a biological sample comprising:

(a) contacting the sample with one or more nucleic acids of claim 1, under conditions such that hybridization occurs, and

(b) detecting hybridization of said nucleic acids to the one or more *Borrelia* nucleic acid sequences present in the biological sample.

19. A method of detecting *Borrelia* nucleic acids in a biological sample obtained from an animal, comprising:

(a) amplifying one or more *Borrelia* nucleic acid sequences in said sample using polymerase chain reaction, and
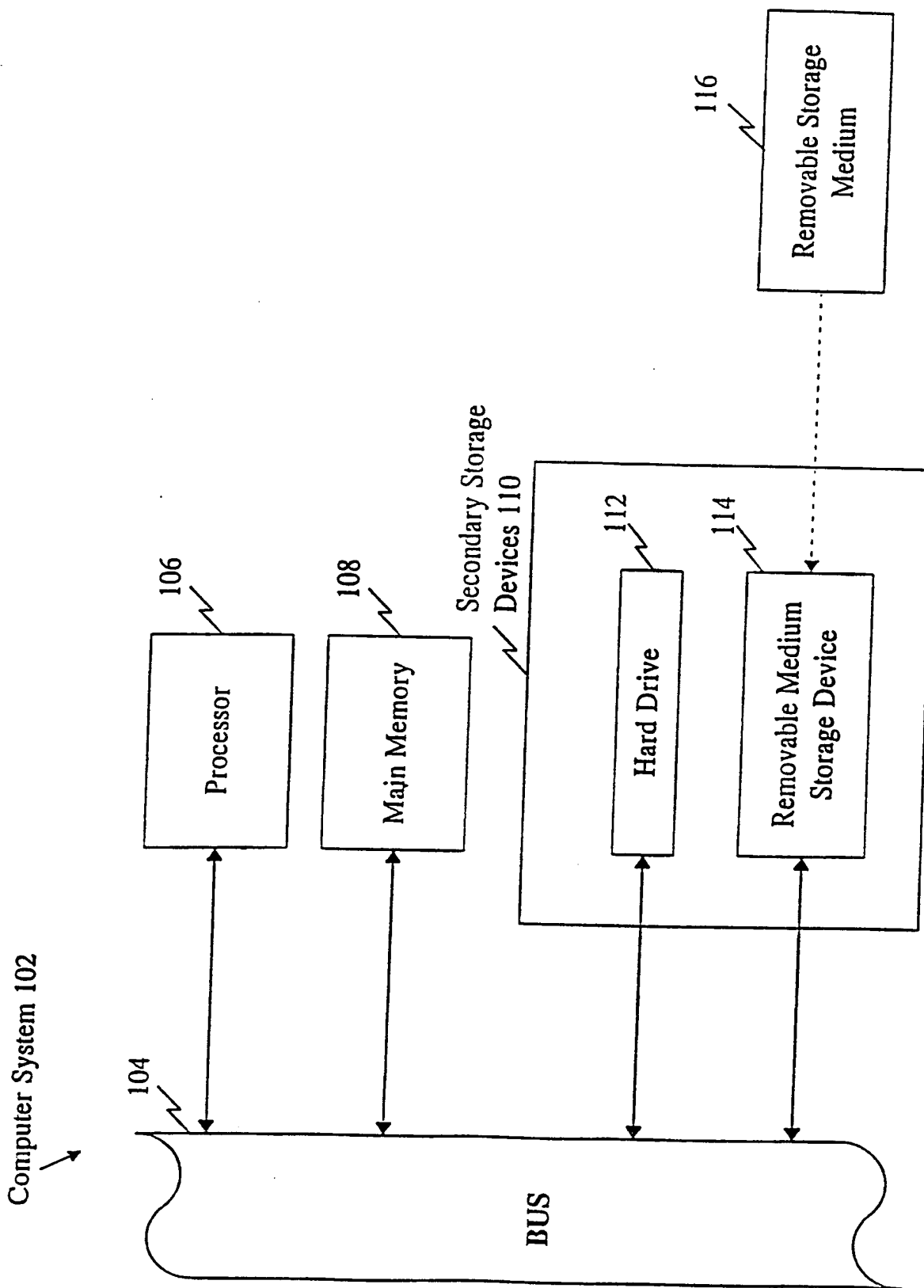
(b) detecting said amplified *Borrelia* nucleic acid.

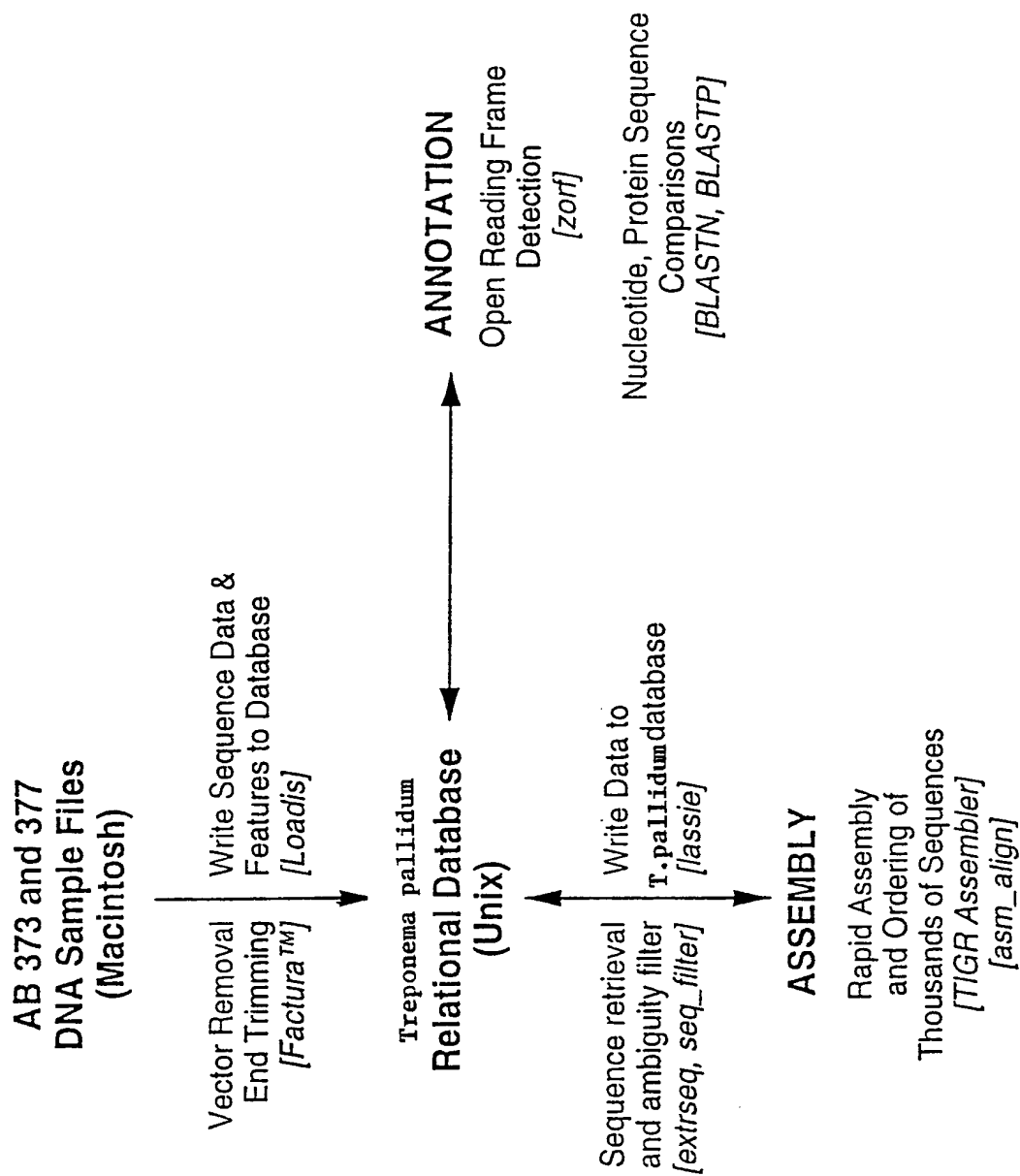20. A kit for detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

(a) a polypeptide of claim 9 attached to a solid support; and

(b) detecting means.

21. A method of detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

(a) contacting the sample with a polypeptide of claim 9; and

(b) detecting antibody-antigen complexes.

Figure 1

Figure 2

AB 373 and 377
DNA Sample Files
(Macintosh)

Vector Removal
End Trimming
[Factura™]

Write Sequence Data &
Features to Database
[Loadis]

Treponema pallidum
Relational Database
(Unix)

ANNOTATION

Open Reading Frame
Detection
[zorf]

Nucleotide, Protein Sequence
Comparisons
[BLASTN, BLASTP]

Sequence retrieval
and ambiguity filter
[extrseq, seq_filter]

Write Data to
T.pallidum database
[lassie]

ASSEMBLY

Rapid Assembly
and Ordering of
Thousands of Sequences
[TIGR Assembler]
[asm_align]

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/02, 2/04; C12N 5/00, 5/10, 15/00, 15/09, 15/11, 15/31
US CL :435/69.1, 71.1, 172.3; 536/23.1, 23.7. 24.3, 24.32

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 71.1, 172.3; 536/23.1, 23.7. 24.3, 24.32

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BARBOUR, A.G. et al. The nucleotide sequence of a linear plasmid of Borrelia burgdorferi reveals similarities to those of circular plasmids of other prokaryotes. Journal of Bacteriology. 1996, Vol. 178, No. 22, pages 6635-6639, see entire document, especially sequences.	1-3, 5-8, and 14
Y,P	FRASER, C.M. et al. Genomic Sequence of a Lyme disease spirochaete, Borrelia burgdorferi. Nature. 11 December 1997, Vol. 390, pages 580-586, see entire document, especially sequences.	1-3, 5-8, and 14

☐ Further documents are listed in the continuation of Box C.   ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier document published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		
		"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure. use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
21 SEPTEMBER 1998	16 OCT 1998

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	BRIAN R. STANTON
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US98/12764

Box I   Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 4
   because they relate to subject matter not required to be searched by this Authority, namely:

   Please See Extra Sheet.

2. ☐ Claims Nos.:
   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II   Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

   Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
   1-3, 5-8, and 14

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1))(July 1992)★

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

Databases: Genbank, APS
Search Terms: sequence search of claimed sequences including only first, middle, and last 100 bases of each of the first ten sequences; open; read?; frame?; orf; protein?; borrelia?

BOX I. OBSERVATIONS WHERE CLAIMS WERE FOUND UNSEARCHABLE
1. Subject matter not required to be searched by this ISA, namely:

The subject matter of claim 4 is directed to a "computer readable medium" having recorded thereon nucleotide sequence information. However, under PCT Rule 39, the International Searching Authority is not required to search an invention that is drawn to "mere presentations of information" (See Rule 39.1 (v)). Therefore, claim 4 has not been considered by this authority.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1.

Group I:

Claims 1-3, 5-8, and 14, drawn to a polynucleotide selected from SEQ ID NOs 1-155 and associated vectors, host cells, and methods of making proteins. This group includes the first method making the claimed vectors (claim 5) and the first method of use of the cells (claim 8) to make a product. There are a total of 155 polynucleotide sequences of which the first 10 are selected for examination and therefore, there are 37 remaining additional groups of 4 polynucleotide sequences.

Group II:

Claims 9, 11-13, and 16, drawn to polypeptides and/or fragments thereof with the amino acid sequence defined by SEQ ID NOs 1-155. Within this group there are a total of 155 polypeptide sequences and therefore 154 additional species of proteins.

Group III:

Claims 10 and 15, drawn to an antibody that binds to a polypeptide with the amino acid sequence defined by SEQ ID NOs:1-155. Within this group there are a total of 155 antibodies and therefore 154 additional species of antibody proteins.

Group IV:

Claim 17, drawn to a process of preventing, treating, or attenuating and infection caused by a member of the Borrelia genus by administering a polypeptide of group II which is a second/alternative process of use of the second product.

In Group IV, and where additional fees are paid, the claims are searched only insofar as they are applicable to the selected polypeptide as the first species as directed to a process practiced using a polypeptide. There are 154 additional polypeptide species of proteins.

Group V:

Claim 18 and 19, drawn to a method of detection of a Borrelia nucleic acid using the nucleic acids of the invention of group I. This method is a second process of use of the first claimed product in Group I. Additionally Group V contains indica that there are a total of 155 polynucleotide sequences and therefore, nine(9) additional groups of four (4) polynucleotide sequences beyond the first ten (10) sequences.

Group VI:

Claims 20 and 21, drawn to a method of detecting antibodies in biological samples using the proteins of the

invention of group II. This is an alternative process of use of the polypeptides. There appear to be a total of 155 polypeptide sequences and therefore 154 additional species of the use f these proteins.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Claims of Group I are drawn to nucleotides, nucleotide constructs, and/or methods requiring the use of nucleotides or nucleotide constructs that contain more than ten individual, independent, and distinct nucleotide sequences in alternative form. Accordingly, these claims are subject to lack of unity as outlined in 1192 O.G. 68 (19 November 1996).

For Group I, the first ten (10) of the individual polynucleotide sequences are designated as SEQ ID NOs 1-10. The search of the no more than ten sequences may include the complements of the selected sequences and, where appropriate, may include subsequences within the selected sequences (e.g., oligomeric probes and/or primers). Similarly, the invention of Group V encompasses the use of multiple independent and distinct proteins that are encompassed within the referenced O.G. notice.

In Group II-IV and VI (as directed to the species which are polynucleotides or antibodies) should applicant pay the additional fee for the examination/search of any of these inventions, additional fees will be required for consideration of each of the species of proteins and/or antibodies after the first of each.

Where Applicant may elect to pay additional fees for a search of sequences beyond the initial ten (10) polynucleotide sequences, and in accordance with 1192 O.G. 68 (19 November 1996), applicant may select additional groups of polynucleotides consisting of four (4) sequences beyond the initial ten (10) sequences for Group I which would then be searched with Group I upon payment of the requisite fees for the requisite Groups beyond Group I.

As to the polypeptides and antibodies of Groups II, III, IV and VI, (as directed to different species of polypeptides and antibodies) each is a distinct and different protein with no requisite structural or functional relationship.

The special technical feature of the invention of group I is directed to nucleic acids that are prepared from a bacterial genome. This special technical feature encompasses nucleic acids that are not *per se* required to encode proteins and may be used in multiple independent manners. For example, the nucleic acids may be used as probes to detect bacterial infections. In contrast, the special technical feature of the inventions of groups II-IV and VI encompass proteins and antibodies which are materially distinct molecules with no functional or structural relationship with the claimed nucleic acids. Similarly, multiple uses of the claimed nucleic acids are claimed (see groups I and V) and such bear no requisite structural linkage. For example, the invention of group I requires the use of nucleic acids that encode proteins whereas the invention of group v only requires that organisms contain sequences that hybridize with those claimed.

Therefore, the separately claimed compositions and methods of using such are not so linked by any single special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.